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(54) Title: COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE			
(57) Abstract Compositions and methods for the therapy and diagnosis of cancer, such as breast cancer, are disclosed. Compositions may comprise one or more breast tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a breast tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as breast cancer. Diagnostic methods based on detecting a breast tumor protein, or mRNA encoding such a protein, in a sample are also provided.			

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**COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS
OF BREAST CANCER AND METHODS FOR THEIR USE**

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of breast cancer. The invention is more particularly related to polypeptides comprising at least a portion of a protein that is preferentially expressed in breast tumor tissue and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for treatment of breast cancer.

BACKGROUND OF THE INVENTION

Breast cancer is a significant health problem for women in the United States and throughout the world. Although advances have been made in detection and treatment of the disease, breast cancer remains the second leading cause of cancer-related deaths in women, affecting more than 180,000 women in the United States each year. For women in North America, the life-time odds of getting breast cancer are one in eight.

No vaccine or other universally successful method for the prevention or treatment of breast cancer is currently available. Management of the disease currently relies on a combination of early diagnosis (through routine breast screening procedures) and aggressive treatment, which may include one or more of a variety of treatments such as surgery, radiotherapy, chemotherapy and hormone therapy. The course of treatment for a particular breast cancer is often selected based on a variety of prognostic parameters, including an analysis of specific tumor markers. See, e.g., Porter-Jordan and Lippman, *Breast Cancer* 8:73-100 (1994). However, the use of established markers often leads to a result that is difficult to interpret, and the high mortality observed in breast cancer patients indicates that improvements are needed in the treatment, diagnosis and prevention of the disease.

Accordingly, there is a need in the art for improved methods for the treatment and diagnosis of breast cancer. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

The present invention provides compounds and methods for the treatment and diagnosis of cancer, such as breast cancer. In one aspect, isolated polypeptides are provided comprising at least a portion of a breast tumor protein or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with protein-specific antisera is not substantially diminished. With certain embodiments, the polypeptide comprises an amino acid sequence encoded by a polynucleotide selected from the group consisting of: (a) nucleotide sequences recited in SEQ ID NO: 1-61, 63-175, 178, 180, 182-313, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468; (b) complements of said nucleotide sequences; and (c) variants of a sequence of (a) or (b). In specific embodiments, the inventive polypeptides comprise at least a portion of a tumor antigen that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 62, 176, 179, 181 and 469-473.

In related aspects, isolated polynucleotides encoding the above polypeptides, or a portion thereof (such as a portion encoding at least 15 contiguous amino acid residues of a breast tumor protein), are provided. In specific embodiments, such polynucleotides comprise a sequence selected from the group consisting of sequences provided in SEQ ID NO: 1-61, 63-175, 178, 180, 182-313, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 and variants thereof. The present invention further provides expression vectors comprising the above polynucleotides, together with host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known breast tumor antigen.

The present invention also provides pharmaceutical compositions comprising at least one of the above polypeptides, or a polynucleotide encoding such a polypeptide, and a physiologically acceptable carrier, together with vaccines. For prophylactic or therapeutic use, comprising at least one such polypeptide or polynucleotide in combination with an immunostimulant. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a breast tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

In yet another aspect, methods are provided for inhibiting the development of breast cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a breast tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a breast tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide;

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a breast tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

The polypeptides disclosed herein may be usefully employed in the diagnosis and monitoring of breast cancer. In one aspect of the present invention, methods are provided for detecting a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; and (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in a patient. In preferred embodiments, the binding agent is an antibody, most preferably a monoclonal antibody. The cancer may be breast cancer.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that is capable of binding to one of the above polypeptides; (b) detecting in the sample an amount of a polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amounts of polypeptide detected in steps (b) and (c).

Within related aspects, the present invention provides antibodies, preferably monoclonal antibodies, that bind to the inventive polypeptides, as well as diagnostic kits comprising such antibodies, and methods of using such antibodies to inhibit the development of breast cancer.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, diagnostic kits comprising the above oligonucleotide probes or primers are provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWING AND SEQUENCE IDENTIFIERS

Fig. 1 shows the results of a Northern blot of the clone SYN18C6 (SEQ ID NO: 40).

SEQ ID NO: 1 is the determined cDNA sequence of JBT2.

SEQ ID NO: 2 is the determined cDNA sequence of JBT6.

SEQ ID NO: 3 is the determined cDNA sequence of JBT7.

SEQ ID NO: 4 is the determined cDNA sequence of JBT10.
SEQ ID NO: 5 is the determined cDNA sequence of JBT13.
SEQ ID NO: 6 is the determined cDNA sequence of JBT14.
SEQ ID NO: 7 is the determined cDNA sequence of JBT15.
SEQ ID NO: 8 is the determined cDNA sequence of JBT16.
SEQ ID NO: 9 is the determined cDNA sequence of JBT17.
SEQ ID NO: 10 is the determined cDNA sequence of JBT22.
SEQ ID NO: 11 is the determined cDNA sequence of JBT25.
SEQ ID NO: 12 is the determined cDNA sequence of JBT28.
SEQ ID NO: 13 is the determined cDNA sequence of JBT32.
SEQ ID NO: 14 is the determined cDNA sequence of JBT33.
SEQ ID NO: 15 is the determined cDNA sequence of JBT34.
SEQ ID NO: 16 is the determined cDNA sequence of JBT36.
SEQ ID NO: 17 is the determined cDNA sequence of JBT37.
SEQ ID NO: 18 is the determined cDNA sequence of JBT51.
SEQ ID NO: 19 is the determined cDNA sequence of JBTT1.
SEQ ID NO: 20 is the determined cDNA sequence of JBTT7.
SEQ ID NO: 21 is the determined cDNA sequence of JBTT11.
SEQ ID NO: 22 is the determined cDNA sequence of JBTT14.
SEQ ID NO: 23 is the determined cDNA sequence of JBTT18.
SEQ ID NO: 24 is the determined cDNA sequence of JBTT19.
SEQ ID NO: 25 is the determined cDNA sequence of JBTT20.
SEQ ID NO: 26 is the determined cDNA sequence of JBTT21.
SEQ ID NO: 27 is the determined cDNA sequence of JBTT22.
SEQ ID NO: 28 is the determined cDNA sequence of JBTT28.
SEQ ID NO: 29 is the determined cDNA sequence of JBTT29.
SEQ ID NO: 30 is the determined cDNA sequence of JBTT33.
SEQ ID NO: 31 is the determined cDNA sequence of JBTT37.
SEQ ID NO: 32 is the determined cDNA sequence of JBTT38.
SEQ ID NO: 33 is the determined cDNA sequence of JBTT47.
SEQ ID NO: 34 is the determined cDNA sequence of JBTT48.

SEQ ID NO: 35 is the determined cDNA sequence of JBTT50.
SEQ ID NO: 36 is the determined cDNA sequence of JBTT51.
SEQ ID NO: 37 is the determined cDNA sequence of JBTT52.
SEQ ID NO: 38 is the determined cDNA sequence of JBTT54.
SEQ ID NO: 39 is the determined cDNA sequence of SYN17F4.
SEQ ID NO: 40 is the determined cDNA sequence of SYN18C6.
SEQ ID NO: 41 is the determined cDNA sequence of SYN19A2.
SEQ ID NO: 42 is the determined cDNA sequence of SYN19C8.
SEQ ID NO: 43 is the determined cDNA sequence of SYN20A12.
SEQ ID NO: 44 is the determined cDNA sequence of SYN20G6.
SEQ ID NO: 45 is the determined cDNA sequence of SYN20G6-2.
SEQ ID NO: 46 is the determined cDNA sequence of SYN21B9.
SEQ ID NO: 47 is the determined cDNA sequence of SYN21B9-2.
SEQ ID NO: 48 is the determined cDNA sequence of SYN21C10.
SEQ ID NO: 49 is the determined cDNA sequence of SYN21G10.
SEQ ID NO: 50 is the determined cDNA sequence of SYN21G10-2.
SEQ ID NO: 51 is the determined cDNA sequence of SYN21G11.
SEQ ID NO: 52 is the determined cDNA sequence of SYN21G11-2.
SEQ ID NO: 53 is the determined cDNA sequence of SYN21H8.
SEQ ID NO: 54 is the determined cDNA sequence of SYN22A10.
SEQ ID NO: 55 is the determined cDNA sequence of SYN22A10-2.
SEQ ID NO: 56 is the determined cDNA sequence of SYN22A12.
SEQ ID NO: 57 is the determined cDNA sequence of SYN22A2.
SEQ ID NO: 58 is the determined cDNA sequence of SYN22B4.
SEQ ID NO: 59 is the determined cDNA sequence of SYN22C2.
SEQ ID NO: 60 is the determined cDNA sequence of SYN22E10.
SEQ ID NO: 61 is the determined cDNA sequence of SYN22F2.
SEQ ID NO: 62 is a predicted amino acid sequence for SYN18C6.
SEQ ID NO: 63 is the determined cDNA sequence of B723P.
SEQ ID NO: 64 is the determined cDNA sequence for B724P.
SEQ ID NO: 65 is the determined cDNA sequence of B770P.

SEQ ID NO: 66 is the determined cDNA sequence of B716P.

SEQ ID NO: 67 is the determined cDNA sequence of B725P.

SEQ ID NO: 68 is the determined cDNA sequence of B717P.

SEQ ID NO: 69 is the determined cDNA sequence of B771P.

SEQ ID NO: 70 is the determined cDNA sequence of B722P.

SEQ ID NO: 71 is the determined cDNA sequence of B726P.

SEQ ID NO: 72 is the determined cDNA sequence of B727P.

SEQ ID NO: 73 is the determined cDNA sequence of B728P.

SEQ ID NO: 74-87 are the determined cDNA sequences of isolated clones which show homology to known sequences.

SEQ ID NO: 88 is the determined cDNA sequence of 13053.

SEQ ID NO: 89 is the determined cDNA sequence of 13057.

SEQ ID NO: 90 is the determined cDNA sequence of 13059.

SEQ ID NO: 91 is the determined cDNA sequence of 13065.

SEQ ID NO: 92 is the determined cDNA sequence of 13067.

SEQ ID NO: 93 is the determined cDNA sequence of 13068.

SEQ ID NO: 94 is the determined cDNA sequence of 13071.

SEQ ID NO: 95 is the determined cDNA sequence of 13072.

SEQ ID NO: 96 is the determined cDNA sequence of 13073.

SEQ ID NO: 97 is the determined cDNA sequence of 13075.

SEQ ID NO: 98 is the determined cDNA sequence of 13078.

SEQ ID NO: 99 is the determined cDNA sequence of 13079.

SEQ ID NO: 100 is the determined cDNA sequence of 13081.

SEQ ID NO: 101 is the determined cDNA sequence of 13082.

SEQ ID NO: 102 is the determined cDNA sequence of 13092.

SEQ ID NO: 103 is the determined cDNA sequence of 13097.

SEQ ID NO: 104 is the determined cDNA sequence of 13101.

SEQ ID NO: 105 is the determined cDNA sequence of 13102.

SEQ ID NO: 106 is the determined cDNA sequence of 13119.

SEQ ID NO: 107 is the determined cDNA sequence of 13131.

SEQ ID NO: 108 is the determined cDNA sequence of 13133.

SEQ ID NO: 109 is the determined cDNA sequence of 13135.
SEQ ID NO: 110 is the determined cDNA sequence of 13139.
SEQ ID NO: 111 is the determined cDNA sequence of 13140.
SEQ ID NO: 112 is the determined cDNA sequence of 13146.
SEQ ID NO: 113 is the determined cDNA sequence of 13147.
SEQ ID NO: 114 is the determined cDNA sequence of 13148.
SEQ ID NO: 115 is the determined cDNA sequence of 13149.
SEQ ID NO: 116 is the determined cDNA sequence of 13151.
SEQ ID NO: 117 is the determined cDNA sequence of 13051
SEQ ID NO: 118 is the determined cDNA sequence of 13052
SEQ ID NO: 119 is the determined cDNA sequence of 13055
SEQ ID NO: 120 is the determined cDNA sequence of 13058
SEQ ID NO: 121 is the determined cDNA sequence of 13062
SEQ ID NO: 122 is the determined cDNA sequence of 13064
SEQ ID NO: 123 is the determined cDNA sequence of 13080
SEQ ID NO: 124 is the determined cDNA sequence of 13093
SEQ ID NO: 125 is the determined cDNA sequence of 13094
SEQ ID NO: 126 is the determined cDNA sequence of 13095
SEQ ID NO: 127 is the determined cDNA sequence of 13096
SEQ ID NO: 128 is the determined cDNA sequence of 13099
SEQ ID NO: 129 is the determined cDNA sequence of 13100
SEQ ID NO: 130 is the determined cDNA sequence of 13103
SEQ ID NO: 131 is the determined cDNA sequence of 13106
SEQ ID NO: 132 is the determined cDNA sequence of 13107
SEQ ID NO: 133 is the determined cDNA sequence of 13108
SEQ ID NO: 134 is the determined cDNA sequence of 13121
SEQ ID NO: 135 is the determined cDNA sequence of 13126
SEQ ID NO: 136 is the determined cDNA sequence of 13129
SEQ ID NO: 137 is the determined cDNA sequence of 13130
SEQ ID NO: 138 is the determined cDNA sequence of 13134
SEQ ID NO: 139 is the determined cDNA sequence of 13141

SEQ ID NO: 140 is the determined cDNA sequence of 13142
SEQ ID NO: 141 is the determined cDNA sequence of 14376
SEQ ID NO: 142 is the determined cDNA sequence of 14377
SEQ ID NO: 143 is the determined cDNA sequence of 14383
SEQ ID NO: 144 is the determined cDNA sequence of 14384
SEQ ID NO: 145 is the determined cDNA sequence of 14387
SEQ ID NO: 146 is the determined cDNA sequence of 14392
SEQ ID NO: 147 is the determined cDNA sequence of 14394
SEQ ID NO: 148 is the determined cDNA sequence of 14398
SEQ ID NO: 149 is the determined cDNA sequence of 14401
SEQ ID NO: 150 is the determined cDNA sequence of 14402
SEQ ID NO: 151 is the determined cDNA sequence of 14405
SEQ ID NO: 152 is the determined cDNA sequence of 14409
SEQ ID NO: 153 is the determined cDNA sequence of 14412
SEQ ID NO: 154 is the determined cDNA sequence of 14414
SEQ ID NO: 155 is the determined cDNA sequence of 14415
SEQ ID NO: 156 is the determined cDNA sequence of 14416
SEQ ID NO: 157 is the determined cDNA sequence of 14419
SEQ ID NO: 158 is the determined cDNA sequence of 14426
SEQ ID NO: 159 is the determined cDNA sequence of 14427
SEQ ID NO: 160 is the determined cDNA sequence of 14375
SEQ ID NO: 161 is the determined cDNA sequence of 14378
SEQ ID NO: 162 is the determined cDNA sequence of 14379
SEQ ID NO: 163 is the determined cDNA sequence of 14380
SEQ ID NO: 164 is the determined cDNA sequence of 14381
SEQ ID NO: 165 is the determined cDNA sequence of 14382
SEQ ID NO: 166 is the determined cDNA sequence of 14388
SEQ ID NO: 167 is the determined cDNA sequence of 14399
SEQ ID NO: 168 is the determined cDNA sequence of 14406
SEQ ID NO: 169 is the determined cDNA sequence of 14407
SEQ ID NO: 170 is the determined cDNA sequence of 14408

SEQ ID NO: 171 is the determined cDNA sequence of 14417

SEQ ID NO: 172 is the determined cDNA sequence of 14418

SEQ ID NO: 173 is the determined cDNA sequence of 14423

SEQ ID NO: 174 is the determined cDNA sequence of 14424

SEQ ID NO: 175 is the determined cDNA sequence of B726P-20

SEQ ID NO: 176 is the predicted amino acid sequence of B726P-20

SEQ ID NO: 177 is a PCR primer

SEQ ID NO: 178 is the determined cDNA sequence of B726P-74

SEQ ID NO: 179 is the predicted amino acid sequence of B726P-74

SEQ ID NO: 180 is the determined cDNA sequence of B726P-79

SEQ ID NO: 181 is the predicted amino acid sequence of B726P-79

SEQ ID NO: 182 is the determined cDNA sequence of 19439.1, showing homology to the mammaglobin gene

SEQ ID NO: 183 is the determined cDNA sequence of 19407.1, showing homology to the human keratin gene

SEQ ID NO: 184 is the determined cDNA sequence of 19428.1, showing homology to human chromosome 17 clone

SEQ ID NO: 185 is the determined cDNA sequence of B808P (19408), showing no significant homology to any known gene

SEQ ID NO: 186 is the determined cDNA sequence of 19460.1, showing no significant homology to any known gene

SEQ ID NO: 187 is the determined cDNA sequence of 19419.1, showing homology to Ig kappa light chain

SEQ ID NO: 188 is the determined cDNA sequence of 19411.1, showing homology to human alpha-1 collagen

SEQ ID NO: 189 is the determined cDNA sequence of 19420.1, showing homology to mus musculus proteinase-3

SEQ ID NO: 190 is the determined cDNA sequence of 19432.1, showing homology to human high motility group box

SEQ ID NO: 191 is the determined cDNA sequence of 19412.1, showing homology to the human plasminogen activator gene

SEQ ID NO: 192 is the determined cDNA sequence of 19415.1, showing homology to mitogen activated protein kinase

SEQ ID NO: 193 is the determined cDNA sequence of 19409.1, showing homology to the chondroitin sulfate proteoglycan protein

SEQ ID NO: 194 is the determined cDNA sequence of 19406.1, showing no significant homology to any known gene

SEQ ID NO: 195 is the determined cDNA sequence of 19421.1, showing homology to human fibronectin

SEQ ID NO: 196 is the determined cDNA sequence of 19426.1, showing homology to the retinoic acid receptor responder 3

SEQ ID NO: 197 is the determined cDNA sequence of 19425.1, showing homology to MyD88 mRNA

SEQ ID NO: 198 is the determined cDNA sequence of 19424.1, showing homology to peptide transporter (TAP-1) mRNA

SEQ ID NO: 199 is the determined cDNA sequence of 19429.1, showing no significant homology to any known gene

SEQ ID NO: 200 is the determined cDNA sequence of 19435.1, showing homology to human polymorphic epithelial mucin

SEQ ID NO: 201 is the determined cDNA sequence of B813P (19434.1), showing homology to human GATA-3 transcription factor

SEQ ID NO: 202 is the determined cDNA sequence of 19461.1, showing homology to the human AP-2 gene

SEQ ID NO: 203 is the determined cDNA sequence of 19450.1, showing homology to DNA binding regulatory factor

SEQ ID NO: 204 is the determined cDNA sequence of 19451.1, showing homology to Na/H exchange regulatory co-factor

SEQ ID NO: 205 is the determined cDNA sequence of 19462.1, showing no significant homology to any known gene

SEQ ID NO: 206 is the determined cDNA sequence of 19455.1, showing homology to human mRNA for histone HAS.Z

SEQ ID NO: 207 is the determined cDNA sequence of 19459.1, showing

homology to PAC clone 179N16

SEQ ID NO: 208 is the determined cDNA sequence of 19464.1, showing no significant homology to any known gene

SEQ ID NO: 209 is the determined cDNA sequence of 19414.1, showing homology to lipophilin B

SEQ ID NO: 210 is the determined cDNA sequence of 19413.1, showing homology to chromosome 17 clone hRPK.209_J_20

SEQ ID NO: 211 is the determined cDNA sequence of 19416.1, showing no significant homology to any known gene

SEQ ID NO: 212 is the determined cDNA sequence of 19437.1, showing homology to human clone 24976 mRNA

SEQ ID NO: 213 is the determined cDNA sequence of 19449.1, showing homology to mouse DNA for PG-M core protein

SEQ ID NO: 214 is the determined cDNA sequence of 19446.1, showing no significant homology to any known gene

SEQ ID NO: 215 is the determined cDNA sequence of 19452.1, showing no significant homology to any known gene

SEQ ID NO: 216 is the determined cDNA sequence of 19483.1, showing no significant homology to any known gene

SEQ ID NO: 217 is the determined cDNA sequence of 19526.1, showing homology to human lipophilin C

SEQ ID NO: 218 is the determined cDNA sequence of 19484.1, showing homology to the secreted cement gland protein XAG-2

SEQ ID NO: 219 is the determined cDNA sequence of 19470.1, showing no significant homology to any known gene

SEQ ID NO: 220 is the determined cDNA sequence of 19469.1, showing homology to the human HLA-DM gene

SEQ ID NO: 221 is the determined cDNA sequence of 19482.1, showing homology to the human pS2 protein gene

SEQ ID NO: 222 is the determined cDNA sequence of B805P (19468.1), showing no significant homology to any known gene

SEQ ID NO: 223 is the determined cDNA sequence of 19467.1, showing homology to human thrombospondin mRNA

SEQ ID NO: 224 is the determined cDNA sequence of 19498.1, showing homology to the CDC2 gene involved in cell cycle control

SEQ ID NO: 225 is the determined cDNA sequence of 19506.1, showing homology to human cDNA for TREB protein

SEQ ID NO: 226 is the determined cDNA sequence of B806P (19505.1), showing no significant homology to any known gene

SEQ ID NO: 227 is the determined cDNA sequence of 19486.1, showing homology to type I epidermal keratin

SEQ ID NO: 228 is the determined cDNA sequence of 19510.1, showing homology to glucose transporter for glycoprotein

SEQ ID NO: 229 is the determined cDNA sequence of 19512.1, showing homology to the human lysyl hydroxylase gene

SEQ ID NO: 230 is the determined cDNA sequence of 19511.1, showing homology to human palmitoyl-protein thioesterase

SEQ ID NO: 231 is the determined cDNA sequence of 19508.1, showing homology to human alpha enolase

SEQ ID NO: 232 is the determined cDNA sequence of B807P (19509.1), showing no significant homology to any known gene

SEQ ID NO: 233 is the determined cDNA sequence of B809P (19520.1), showing homology to clone 102D24 on chromosome 11q13.31

SEQ ID NO: 234 is the determined cDNA sequence of 19507.1, showing homology to prosome beta-subunit

SEQ ID NO: 235 is the determined cDNA sequence of 19525.1, showing homology to human pro-urokinase precursor

SEQ ID NO: 236 is the determined cDNA sequence of 19513.1, showing no significant homology to any known gene

SEQ ID NO: 237 is the determined cDNA sequence of 19517.1, showing homology to human PAC 128M19 clone

SEQ ID NO: 238 is the determined cDNA sequence of 19564.1, showing

homology to human cytochrome P450-IIIB

SEQ ID NO: 239 is the determined cDNA sequence of 19553.1, showing homology to human GABA-A receptor pi subunit

SEQ ID NO: 240 is the determined cDNA sequence of B811P (19575.1), showing no significant homology to any known gene

SEQ ID NO: 241 is the determined cDNA sequence of B810P (19560.1), showing no significant homology to any known gene

SEQ ID NO: 242 is the determined cDNA sequence of 19588.1, showing homology to aortic carboxypeptidase-like protein

SEQ ID NO: 243 is the determined cDNA sequence of 19551.1, showing homology to human BCL-1 gene

SEQ ID NO: 244 is the determined cDNA sequence of 19567.1, showing homology to human proteasome-related mRNA

SEQ ID NO: 245 is the determined cDNA sequence of B803P (19583.1), showing no significant homology to any known gene

SEQ ID NO: 246 is the determined cDNA sequence of B812P (19587.1), showing no significant homology to any known gene

SEQ ID NO: 247 is the determined cDNA sequence of B802P (19392.2), showing homology to human chromosome 17

SEQ ID NO: 248 is the determined cDNA sequence of 19393.2, showing homology to human nicein B2 chain

SEQ ID NO: 249 is the determined cDNA sequence of 19398.2, human MHC class II DQ alpha mRNA

SEQ ID NO: 250 is the determined cDNA sequence of B804P (19399.2), showing homology to human Xp22 BAC GSHB-184P14

SEQ ID NO: 251 is the determined cDNA sequence of 19401.2, showing homology to human ikB kinase-b gene

SEQ ID NO: 252 is the determined cDNA sequence of 20266, showing no significant homology to any known gene

SEQ ID NO: 253 is the determined cDNA sequence of B826P (20270), showing no significant homology to any known gene

SEQ ID NO: 254 is the determined cDNA sequence of 20274, showing no significant homology to any known gene

SEQ ID NO: 255 is the determined cDNA sequence of 20276, showing no significant homology to any known gene

SEQ ID NO: 256 is the determined cDNA sequence of 20277, showing no significant homology to any known gene

SEQ ID NO: 257 is the determined cDNA sequence of B823P (20280), showing no significant homology to any known gene

SEQ ID NO: 258 is the determined cDNA sequence of B821P (20281), showing no significant homology to any known gene

SEQ ID NO: 259 is the determined cDNA sequence of B824P (20294), showing no significant homology to any known gene

SEQ ID NO: 260 is the determined cDNA sequence of 20303, showing no significant homology to any known gene

SEQ ID NO: 261 is the determined cDNA sequence of B820P (20310), showing no significant homology to any known gene

SEQ ID NO: 262 is the determined cDNA sequence of B825P (20336), showing no significant homology to any known gene

SEQ ID NO: 263 is the determined cDNA sequence of B827P (20341), showing no significant homology to any known gene

SEQ ID NO: 264 is the determined cDNA sequence of 20941, showing no significant homology to any known gene

SEQ ID NO: 265 is the determined cDNA sequence of 20954, showing no significant homology to any known gene

SEQ ID NO: 266 is the determined cDNA sequence of 20961, showing no significant homology to any known gene

SEQ ID NO: 267 is the determined cDNA sequence of 20965, showing no significant homology to any known gene

SEQ ID NO: 268 is the determined cDNA sequence of 20975, showing no significant homology to any known gene

SEQ ID NO: 269 is the determined cDNA sequence of 20261, showing

homology to Human p120 catenin

SEQ ID NO: 270 is the determined cDNA sequence of B822P (20262), showing homology to Human membrane glycoprotein 4F2

SEQ ID NO: 271 is the determined cDNA sequence of 20265, showing homology to Human Na, K-ATPase Alpha 1

SEQ ID NO: 272 is the determined cDNA sequence of 20267, showing homology to Human heart HS 90, partial cds

SEQ ID NO: 273 is the determined cDNA sequence of 20268, showing homology to Human mRNA GPI-anchored protein p137

SEQ ID NO: 274 is the determined cDNA sequence of 20271, showing homology to Human cleavage stimulation factor 77 kDa subunit

SEQ ID NO: 275 is the determined cDNA sequence of 20272, showing homology to Human p190-B

SEQ ID NO: 276 is the determined cDNA sequence of 20273, showing homology to Human ribophorin

SEQ ID NO: 277 is the determined cDNA sequence of 20278, showing homology to Human ornithine amino transferase

SEQ ID NO: 278 is the determined cDNA sequence of 20279, showing homology to Human S-adenosylmethionine synthetase

SEQ ID NO: 279 is the determined cDNA sequence of 20293, showing homology to Human x inactivation transcript

SEQ ID NO: 280 is the determined cDNA sequence of 20300, showing homology to Human cytochrome p450

SEQ ID NO: 281 is the determined cDNA sequence of 20305, showing homology to Human elongation factor-1 alpha

SEQ ID NO: 282 is the determined cDNA sequence of 20306, showing homology to Human epithelial ets protein

SEQ ID NO: 283 is the determined cDNA sequence of 20307, showing homology to Human signal transducer mRNA

SEQ ID NO: 284 is the determined cDNA sequence of 20313, showing homology to Human GABA-A receptor pi subunit mRNA

SEQ ID NO: 285 is the determined cDNA sequence of 20317, showing homology to Human tyrosine phosphatase

SEQ ID NO: 286 is the determined cDNA sequence of 20318, showing homology to Human cathepsine B proteinase

SEQ ID NO: 287 is the determined cDNA sequence of 20320, showing homology to Human 2-phosphopyruvate-hydratase-alpha-enolase

SEQ ID NO: 288 is the determined cDNA sequence of 20321, showing homology to Human E-cadherin

SEQ ID NO: 289 is the determined cDNA sequence of 20322, showing homology to Human hsp86

SEQ ID NO: 290 is the determined cDNA sequence of B828P (20326), showing homology to Human x inactivation transcript

SEQ ID NO: 291 is the determined cDNA sequence of 20333, showing homology to Human chromatin regulator, SMARCA5

SEQ ID NO: 292 is the determined cDNA sequence of 20335, showing homology to Human sphingolipid activator protein 1

SEQ ID NO: 293 is the determined cDNA sequence of 20337, showing homology to Human hepatocyte growth factor activator inhibitor type 2

SEQ ID NO: 294 is the determined cDNA sequence of 20338, showing homology to Human cell adhesion molecule CD44

SEQ ID NO: 295 is the determined cDNA sequence of 20340, showing homology to Human nuclear factor (erythroid-derived)-like 1

SEQ ID NO: 296 is the determined cDNA sequence of 20938, showing homology to Human vinculin mRNA

SEQ ID NO: 297 is the determined cDNA sequence of 20939, showing homology to Human elongation factor EF-1-alpha

SEQ ID NO: 298 is the determined cDNA sequence of 20940, showing homology to Human nestin gene

SEQ ID NO: 299 is the determined cDNA sequence of 20942, showing homology to Human pancreatic ribonuclease

SEQ ID NO: 300 is the determined cDNA sequence of 20943, showing

homology to Human transcobalamin I

SEQ ID NO: 301 is the determined cDNA sequence of 20944, showing homology to Human beta-tubulin

SEQ ID NO: 302 is the determined cDNA sequence of 20946, showing homology to Human HS1 protein

SEQ ID NO: 303 is the determined cDNA sequence of 20947, showing homology to Human cathepsin B

SEQ ID NO: 304 is the determined cDNA sequence of 20948, showing homology to Human testis enhanced gene transcript

SEQ ID NO: 305 is the determined cDNA sequence of 20949, showing homology to Human elongation factor EF-1-alpha

SEQ ID NO: 306 is the determined cDNA sequence of 20950, showing homology to Human ADP-ribosylation factor 3

SEQ ID NO: 307 is the determined cDNA sequence of 20951, showing homology to Human IFP53 or WRS for tryptophanyl-tRNA synthetase

SEQ ID NO: 308 is the determined cDNA sequence of 20952, showing homology to Human cyclin-dependent protein kinase

SEQ ID NO: 308 is the determined cDNA sequence of 20957, showing homology to Human alpha-tubulin sioform 1

SEQ ID NO: 309 is the determined cDNA sequence of 20959, showing homology to Human tyrosine phosphatase-61bp deletion

SEQ ID NO: 310 is the determined cDNA sequence of 20966, showing homology to Human tyrosine phosphatase

SEQ ID NO: 311 is the determined cDNA sequence of B830P (20976), showing homology to Human nuclear factor NF 45

SEQ ID NO: 312 is the determined cDNA sequence of B829P (20977), showing homology to Human delta-6 fatty acid desaturase

SEQ ID NO: 313 is the determined cDNA sequence of 20978, showing homology to Human nuclear aconitase

SEQ ID NO: 314 is the determined cDNA sequence of 19465, showing no significant homology to any known gene.

SEQ ID NO: 315 is the determined cDNA sequence of clone 23176.
SEQ ID NO: 316 is the determined cDNA sequence of clone 23140.
SEQ ID NO: 317 is the determined cDNA sequence of clone 23166.
SEQ ID NO: 318 is the determined cDNA sequence of clone 23167.
SEQ ID NO: 319 is the determined cDNA sequence of clone 23177.
SEQ ID NO: 320 is the determined cDNA sequence of clone 23217.
SEQ ID NO: 321 is the determined cDNA sequence of clone 23169.
SEQ ID NO: 322 is the determined cDNA sequence of clone 23160.
SEQ ID NO: 323 is the determined cDNA sequence of clone 23182.
SEQ ID NO: 324 is the determined cDNA sequence of clone 23232.
SEQ ID NO: 325 is the determined cDNA sequence of clone 23203.
SEQ ID NO: 326 is the determined cDNA sequence of clone 23198.
SEQ ID NO: 327 is the determined cDNA sequence of clone 23224.
SEQ ID NO: 328 is the determined cDNA sequence of clone 23142.
SEQ ID NO: 329 is the determined cDNA sequence of clone 23138.
SEQ ID NO: 330 is the determined cDNA sequence of clone 23147.
SEQ ID NO: 331 is the determined cDNA sequence of clone 23148.
SEQ ID NO: 332 is the determined cDNA sequence of clone 23149.
SEQ ID NO: 333 is the determined cDNA sequence of clone 23172.
SEQ ID NO: 334 is the determined cDNA sequence of clone 23158.
SEQ ID NO: 335 is the determined cDNA sequence of clone 23156.
SEQ ID NO: 336 is the determined cDNA sequence of clone 23221.
SEQ ID NO: 337 is the determined cDNA sequence of clone 23223.
SEQ ID NO: 338 is the determined cDNA sequence of clone 23155.
SEQ ID NO: 339 is the determined cDNA sequence of clone 23225.
SEQ ID NO: 340 is the determined cDNA sequence of clone 23226.
SEQ ID NO: 341 is the determined cDNA sequence of clone 23228.
SEQ ID NO: 342 is the determined cDNA sequence of clone 23229.
SEQ ID NO: 343 is the determined cDNA sequence of clone 23231.
SEQ ID NO: 344 is the determined cDNA sequence of clone 23154.
SEQ ID NO: 345 is the determined cDNA sequence of clone 23157.

SEQ ID NO: 346 is the determined cDNA sequence of clone 23153.
SEQ ID NO: 347 is the determined cDNA sequence of clone 23159.
SEQ ID NO: 348 is the determined cDNA sequence of clone 23152.
SEQ ID NO: 349 is the determined cDNA sequence of clone 23161.
SEQ ID NO: 350 is the determined cDNA sequence of clone 23162.
SEQ ID NO: 351 is the determined cDNA sequence of clone 23163.
SEQ ID NO: 352 is the determined cDNA sequence of clone 23164.
SEQ ID NO: 353 is the determined cDNA sequence of clone 23165.
SEQ ID NO: 354 is the determined cDNA sequence of clone 23151.
SEQ ID NO: 355 is the determined cDNA sequence of clone 23150.
SEQ ID NO: 356 is the determined cDNA sequence of clone 23168.
SEQ ID NO: 357 is the determined cDNA sequence of clone 23146.
SEQ ID NO: 358 is the determined cDNA sequence of clone 23170.
SEQ ID NO: 359 is the determined cDNA sequence of clone 23171.
SEQ ID NO: 360 is the determined cDNA sequence of clone 23145.
SEQ ID NO: 361 is the determined cDNA sequence of clone 23174.
SEQ ID NO: 362 is the determined cDNA sequence of clone 23175.
SEQ ID NO: 363 is the determined cDNA sequence of clone 23144.
SEQ ID NO: 364 is the determined cDNA sequence of clone 23178.
SEQ ID NO: 365 is the determined cDNA sequence of clone 23179.
SEQ ID NO: 366 is the determined cDNA sequence of clone 23180.
SEQ ID NO: 367 is the determined cDNA sequence of clone 23181.
SEQ ID NO: 368 is the determined cDNA sequence of clone 23143
SEQ ID NO: 369 is the determined cDNA sequence of clone 23183.
SEQ ID NO: 370 is the determined cDNA sequence of clone 23184.
SEQ ID NO: 371 is the determined cDNA sequence of clone 23185.
SEQ ID NO: 372 is the determined cDNA sequence of clone 23186.
SEQ ID NO: 373 is the determined cDNA sequence of clone 23187.
SEQ ID NO: 374 is the determined cDNA sequence of clone 23190.
SEQ ID NO: 375 is the determined cDNA sequence of clone 23189.
SEQ ID NO: 376 is the determined cDNA sequence of clone 23202.

SEQ ID NO: 378 is the determined cDNA sequence of clone 23191.
SEQ ID NO: 379 is the determined cDNA sequence of clone 23188.
SEQ ID NO: 380 is the determined cDNA sequence of clone 23194.
SEQ ID NO: 381 is the determined cDNA sequence of clone 23196.
SEQ ID NO: 382 is the determined cDNA sequence of clone 23195.
SEQ ID NO: 383 is the determined cDNA sequence of clone 23193.
SEQ ID NO: 384 is the determined cDNA sequence of clone 23199.
SEQ ID NO: 385 is the determined cDNA sequence of clone 23200.
SEQ ID NO: 386 is the determined cDNA sequence of clone 23192.
SEQ ID NO: 387 is the determined cDNA sequence of clone 23201.
SEQ ID NO: 388 is the determined cDNA sequence of clone 23141.
SEQ ID NO: 389 is the determined cDNA sequence of clone 23139.
SEQ ID NO: 390 is the determined cDNA sequence of clone 23204.
SEQ ID NO: 391 is the determined cDNA sequence of clone 23205.
SEQ ID NO: 392 is the determined cDNA sequence of clone 23206.
SEQ ID NO: 393 is the determined cDNA sequence of clone 23207.
SEQ ID NO: 394 is the determined cDNA sequence of clone 23208.
SEQ ID NO: 395 is the determined cDNA sequence of clone 23209.
SEQ ID NO: 396 is the determined cDNA sequence of clone 23210.
SEQ ID NO: 397 is the determined cDNA sequence of clone 23211.
SEQ ID NO: 398 is the determined cDNA sequence of clone 23212.
SEQ ID NO: 399 is the determined cDNA sequence of clone 23214.
SEQ ID NO: 400 is the determined cDNA sequence of clone 23215.
SEQ ID NO: 401 is the determined cDNA sequence of clone 23216.
SEQ ID NO: 402 is the determined cDNA sequence of clone 23137.
SEQ ID NO: 403 is the determined cDNA sequence of clone 23218.
SEQ ID NO: 404 is the determined cDNA sequence of clone 23220.
SEQ ID NO: 405 is the determined cDNA sequence of clone 19462.
SEQ ID NO: 406 is the determined cDNA sequence of clone 19430.
SEQ ID NO: 407 is the determined cDNA sequence of clone 19407.
SEQ ID NO: 408 is the determined cDNA sequence of clone 19448.

SEQ ID NO: 409 is the determined cDNA sequence of clone 19447.
SEQ ID NO: 410 is the determined cDNA sequence of clone 19426.
SEQ ID NO: 411 is the determined cDNA sequence of clone 19441.
SEQ ID NO: 412 is the determined cDNA sequence of clone 19454.
SEQ ID NO: 413 is the determined cDNA sequence of clone 19463.
SEQ ID NO: 414 is the determined cDNA sequence of clone 19419.
SEQ ID NO: 415 is the determined cDNA sequence of clone 19434.
SEQ ID NO: 416 is the determined extended cDNA sequence of B820P.
SEQ ID NO: 417 is the determined extended cDNA sequence of B821P.
SEQ ID NO: 418 is the determined extended cDNA sequence of B822P.
SEQ ID NO: 419 is the determined extended cDNA sequence of B823P.
SEQ ID NO: 420 is the determined extended cDNA sequence of B824P.
SEQ ID NO: 421 is the determined extended cDNA sequence of B825P.
SEQ ID NO: 422 is the determined extended cDNA sequence of B826P.
SEQ ID NO: 423 is the determined extended cDNA sequence of B827P.
SEQ ID NO: 424 is the determined extended cDNA sequence of B828P.
SEQ ID NO: 425 is the determined extended cDNA sequence of B829P.
SEQ ID NO: 426 is the determined extended cDNA sequence of B830P.
SEQ ID NO: 427 is the determined cDNA sequence of clone 266B4.
SEQ ID NO: 428 is the determined cDNA sequence of clone 22892.
SEQ ID NO: 429 is the determined cDNA sequence of clone 266G3.
SEQ ID NO: 430 is the determined cDNA sequence of clone 22890.
SEQ ID NO: 431 is the determined cDNA sequence of clone 264B4.
SEQ ID NO: 432 is the determined cDNA sequence of clone 22883.
SEQ ID NO: 433 is the determined cDNA sequence of clone 22882.
SEQ ID NO: 434 is the determined cDNA sequence of clone 22880.
SEQ ID NO: 435 is the determined cDNA sequence of clone 263G1.
SEQ ID NO: 436 is the determined cDNA sequence of clone 263G6.
SEQ ID NO: 437 is the determined cDNA sequence of clone 262B2.
SEQ ID NO: 438 is the determined cDNA sequence of clone 262B6.
SEQ ID NO: 439 is the determined cDNA sequence of clone 22869.

SEQ ID NO: 440 is the determined cDNA sequence of clone 21374.

SEQ ID NO: 441 is the determined cDNA sequence of clone 21362.

SEQ ID NO: 442 is the determined cDNA sequence of clone 21349.

SEQ ID NO: 443 is the determined cDNA sequence of clone 21309.

SEQ ID NO: 444 is the determined cDNA sequence of clone 21097.

SEQ ID NO: 445 is the determined cDNA sequence of clone 21096.

SEQ ID NO: 446 is the determined cDNA sequence of clone 21094.

SEQ ID NO: 447 is the determined cDNA sequence of clone 21093.

SEQ ID NO: 448 is the determined cDNA sequence of clone 21091.

SEQ ID NO: 449 is the determined cDNA sequence of clone 21089.

SEQ ID NO: 450 is the determined cDNA sequence of clone 21087.

SEQ ID NO: 451 is the determined cDNA sequence of clone 21085.

SEQ ID NO: 452 is the determined cDNA sequence of clone 21084.

SEQ ID NO: 453 is a first partial cDNA sequence of clone 2BT1-40.

SEQ ID NO: 454 is a second partial cDNA sequence of clone 2BT1-40.

SEQ ID NO: 455 is the determined cDNA sequence of clone 21063.

SEQ ID NO: 456 is the determined cDNA sequence of clone 21062.

SEQ ID NO: 457 is the determined cDNA sequence of clone 21060.

SEQ ID NO: 458 is the determined cDNA sequence of clone 21053.

SEQ ID NO: 459 is the determined cDNA sequence of clone 21050.

SEQ ID NO: 460 is the determined cDNA sequence of clone 21036.

SEQ ID NO: 461 is the determined cDNA sequence of clone 21037.

SEQ ID NO: 462 is the determined cDNA sequence of clone 21048.

SEQ ID NO: 463 is a consensus DNA sequence of B726P (referred to as B726P-spliced_seq_B726P).

SEQ ID NO: 464 is the determined cDNA sequence of a second splice form of B726P (referred to as 27490.seq_B726P).

SEQ ID NO: 465 is the determined cDNA sequence of a third splice form of B726P (referred to as 27068.seq_B726P).

SEQ ID NO: 466 is the determined cDNA sequence of a second splice form of B726P (referred to as 23113.seq_B726P).

SEQ ID NO: 467 is the determined cDNA sequence of a second splice form of B726P (referred to as 23103.seq_B726P).

SEQ ID NO: 468 is the determined cDNA sequence of a second splice form of B726P (referred to as 19310.seq_B726P).

SEQ ID NO: 469 is the predicted amino acid sequence encoded by the upstream ORF of SEQ ID NO: 463.

SEQ ID NO: 470 is the predicted amino acid sequence encoded by SEQ ID NO: 464.

SEQ ID NO: 471 is the predicted amino acid sequence encoded by SEQ ID NO: 465.

SEQ ID NO: 472 is the predicted amino acid sequence encoded by SEQ ID NO: 466.

SEQ ID NO: 473 is the predicted amino acid sequence encoded by SEQ ID NO: 467.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as breast cancer. The compositions described herein may include breast tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (e.g., T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a breast tumor protein or a variant thereof. A "breast tumor protein" is a protein that is expressed in breast tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain breast tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with breast cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of

binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human breast tumor proteins. Sequences of polynucleotides encoding specific tumor proteins are provided in SEQ ID NOS:1-175, 178, 180 and 182-468.

BREAST TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a breast tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a breast tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a breast tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a breast tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide

sequence that encodes a native breast tumor protein or a portion thereof. The term "variants" also encompasses homologous genes of xenogenic origin.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two

sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.* the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native breast tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a breast tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially

as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as breast tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a breast tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed

using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

Certain nucleic acid sequences of cDNA molecules encoding portions of breast tumor proteins are provided in SEQ ID NO: 1-175, 178, 180 and 182-468. The

isolation of these sequences is described in detail below.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (see Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a breast tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (e.g., by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a breast tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and

still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybudosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (e.g., avian pox virus). The polynucleotides may also be administered as naked plasmid vectors. Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

BREAST TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a breast tumor protein or a variant thereof, as described herein. As noted above, a "breast tumor protein" is a protein that is expressed by breast tumor cells. Proteins that are breast tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with breast cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is

recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a breast tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native breast tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native breast tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native breast tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially

diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, higher eukaryotic and plant cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at

least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al.,

Proc. Natl. Acad. Sci. USA 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (see, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenzae* B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene* 43:265-292, 1986).

LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a breast tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a breast tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a breast tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be

determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as breast cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a breast tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically.

Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane,

Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ⁹⁰Y, ¹²³I, ¹²⁵I, ¹³¹I, ¹⁸⁶Re, ¹⁸⁸Re, ²¹¹At, and ²¹²Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, Pseudomonas exotoxin, Shigella toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and

immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a breast tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the ISOLEX™ system, available from Nexell Therapeutics Inc., Irvine, CA (see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a breast tumor polypeptide, polynucleotide encoding a breast tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a breast tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a breast tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased

rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a breast tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN- γ) is indicative of T cell activation (see Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a breast tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4 $^{+}$ and/or CD8 $^{+}$. Breast tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4 $^{+}$ or CD8 $^{+}$ T cells that proliferate in response to a breast tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a breast tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a breast tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a breast tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant

may be any substance that enhances an immune response to an exogenous antigen. Examples of immunostimulants include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993;

and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants

are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- γ , TNF- α , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT) (see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153,

or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells

or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell

surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (e.g., CD54 and CD11) and costimulatory molecules (e.g., CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a breast tumor protein (or portion or other variant thereof) such that the breast tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the breast tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as breast cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or

following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example,

antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitory, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 µg to 5 mg per kg of

host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (e.g., more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a breast tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more breast tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as breast cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a breast tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length breast tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of

binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g., Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13*).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with breast cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined

by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as breast cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond

to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use breast tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such breast tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a breast tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a breast tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of breast tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a breast tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a breast tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the breast tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a breast tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a breast tumor protein that is at least 10 nucleotides,

and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NOS:1-175, 178, 180 and 182-468. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor.

One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple breast tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a breast tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a breast tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a breast tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a breast tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF BREAST TUMOR POLYPEPTIDES

This Example describes the isolation of breast tumor polypeptides from a breast tumor cDNA library.

A cDNA subtraction library containing cDNA from breast tumor subtracted with normal breast cDNA was constructed as follows. Total RNA was extracted from primary tissues using Trizol reagent (Gibco BRL Life Technologies, Gaithersburg, MD) as described by the manufacturer. The polyA+ RNA was purified using an oligo(dT) cellulose column according to standard protocols. First strand cDNA was synthesized using the primer supplied in a Clontech PCR-Select cDNA Subtraction Kit (Clontech, Palo Alto, CA). The driver DNA consisted of cDNAs from two normal breast tissues with the tester cDNA being from three primary breast tumors. Double-stranded cDNA was synthesized for both tester and driver, and digested with a combination of endonucleases (MluI, MscI, PvuII, SalI and StuI) which recognize six base pairs DNA. This modification increased the average cDNA size dramatically compared with cDNAs generated according to the protocol of Clontech (Palo Alto, CA). The digested tester cDNAs were ligated to two different adaptors and the subtraction was performed according to Clontech's protocol. The subtracted cDNAs were subjected to two rounds of PCR amplification, following the manufacturer's protocol. The resulting PCR products were subcloned into the TA cloning vector, pCRII (Invitrogen, San Diego, CA) and transformed into ElectroMax *E. coli* DH10B cells (Gibco BRL Life, Technologies) by electroporation. DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division (Foster City, CA) Automated Sequencer Model 373A.

Sixty-three distinct cDNA clones were found in the subtracted breast tumor-specific cDNA library. The determined one strand (5' or 3') cDNA sequences for the clones are provided in SEQ ID NO: 1-61, 72 and 73, respectively. Comparison of these cDNA sequences with known sequences in the gene bank using the EMBL and GenBank databases (Release 97) revealed no significant homologies to the sequences provided in SEQ ID NO: 14, 21, 22, 27, 29, 30, 32, 38, 44, 45, 53, 72 and 73. The sequences of SEQ ID NO: 1, 3, 16, 17, 34, 48, 57, 60 and 61 were found to represent known human genes. The sequences of SEQ ID NO: 2, 4, 23, 39 and 50 were found to show some similarity to previously identified non-human genes. The remaining clones (SEQ ID NO: 5-13, 15, 18-20, 24-26, 28, 31, 33, 35-37, 40-43, 46, 47, 49, 51, 52, 54-56, 58 and 59) were found to show at least some degree of homology to previously identified expressed sequence tags (ESTs).

To determine mRNA expression levels of the isolated cDNA clones, cDNA clones from the breast subtraction described above were randomly picked and colony PCR amplified. Their mRNA expression levels in breast tumor, normal breast and various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were arrayed onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. Data was analyzed using Synteni provided GEMTOOLS Software. Of the seventeen cDNA clones examined, those of SEQ ID NO: 40, 46, 59 and 73 were found to be over-expressed in breast tumor and expressed at low levels in all normal tissues tested (breast, PBMC, colon, fetal tissue, salivary gland, bone marrow, lung, pancreas, large intestine, spinal cord, adrenal gland, kidney, pancreas, liver, stomach, skeletal muscle, heart, small intestine, skin, brain and human mammary epithelial cells). The clones of SEQ ID NO: 41 and 48 were found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested, with the exception of bone marrow. The clone of SEQ ID NO: 42 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested except bone marrow and spinal cord. The clone of SEQ ID NO: 43 was

found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of spinal cord, heart and small intestine. The clone of SEQ ID NO: 51 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of large intestine. The clone of SEQ ID NO: 54 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of PBMC, stomach and small intestine. The clone of SEQ ID NO: 56 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of large and small intestine, human mammary epithelia cells and SCID mouse-passaged breast tumor. The clone of SEQ ID NO: 60 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of spinal cord and heart. The clone of SEQ ID NO: 61 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of small intestine. The clone of SEQ ID NO: 72 was found to be over-expressed in breast tumor and expressed at low levels in all other tissues tested with the exception of colon and salivary gland.

The results of a Northern blot analysis of the clone SYN18C6 (SEQ ID NO: 40) are shown in Fig. 1. A predicted protein sequence encoded by SYN18C6 is provided in SEQ ID NO: 62.

Additional cDNA clones that are over-expressed in breast tumor tissue were isolated from breast cDNA subtraction libraries as follows. Breast subtraction libraries were prepared, as described above, by PCR-based subtraction employing pools of breast tumor cDNA as the tester and pools of either normal breast cDNA or cDNA from other normal tissues as the driver. cDNA clones from breast subtraction were randomly picked and colony PCR amplified and their mRNA expression levels in breast tumor, normal breast and various other normal tissues were determined using the microarray technology described above. Twenty-four distinct cDNA clones were found to be over-expressed in breast tumor and expressed at low levels in all normal tissues tested (breast, brain, liver, pancreas, lung, salivary gland, stomach, colon, kidney, bone marrow, skeletal muscle, PBMC, heart, small intestine, adrenal gland, spinal cord, large intestine and skin). The determined partial cDNA sequences for these clones are provided in SEQ ID NO: 63-87. Comparison of the sequences of SEQ ID NO: 74-87

with those in the gene bank as described above, revealed homology to previously identified human genes. No significant homologies were found to the sequences of SEQ ID NO: 63-73.

Three DNA isoforms for the clone B726P (partial sequence provided in SEQ ID NO: 71) were isolated as follows. A radioactive probe was synthesized from B726P by excising B726P DNA from a pT7Blue vector (Novagen) by a BamHI/XbaI restriction digest and using the resulting DNA as the template in a single-stranded PCR in the presence of [α -32P]dCTP. The sequence of the primer employed for this PCR is provided in SEQ ID NO: 177. The resulting radioactive probe was used to probe a directional cDNA library and a random-primed cDNA library made using RNA isolated from breast tumors. Eighty-five clones were identified, excised, purified and sequenced. Of these 85 clones, three were found to each contain a significant open reading frame. The determined cDNA sequence of the isoform B726P-20 is provided in SEQ ID NO: 175, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 176. The determined cDNA sequence of the isoform B726P-74 is provided in SEQ ID NO: 178, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 179. The determined cDNA sequence of the isoform B726P-79 is provided in SEQ ID NO: 180, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 181.

Efforts to obtain a full-length clone of B726P using standard techniques led to the isolation of five additional clones that represent additional 5' sequence of B726P. These clones appear to be alternative splice forms of the same gene. The determined cDNA sequences of these clones are provided in SEQ ID NO: 464-468, with the predicted amino acid sequences encoded by SEQ ID NO: 464-467 being provided in SEQ ID NO: 470-473, respectively. Using standard computer techniques, a 3,681 bp consensus DNA sequence (SEQ ID NO: 463) was created that contains two large open reading frames. The downstream ORF encodes the predicted amino acid sequence of SEQ ID NO: 181. The predicted amino acid sequence encoded by the upstream ORF is provided in SEQ ID NO: 469.

Further isolation of individual clones that are over-expressed in breast tumor tissue was conducted using cDNA subtraction library techniques described above. In particular, a cDNA subtraction library containing cDNA from breast tumors subtracted with five other normal human tissue cDNAs (brain, liver, PBMC, pancreas and normal breast) was utilized in this screening. From the original subtraction, one hundred seventy seven clones were selected to be further characterized by DNA sequencing and microarray analysis. Microarray analysis demonstrated that the sequences in SEQ ID NO: 182-251 were 2 or more fold over-expressed in human breast tumor tissues over normal human tissues. No significant homologies were found for nineteen of these clones, including, SEQ ID NO: 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245 and 246, with the exception of some previously identified expressed sequence tags (ESTs). The remaining clones share some homology to previously identified genes, specifically SEQ ID NO: 181-184, 187-193, 195-198, 200-204, 206, 207, 209, 210, 212, 213, 217, 218, 220, 221, 223-225, 227-231, 233-235, 237-239, 242-244 and 247-251.

Of the seventy clones showing over-expression in breast tumor tissues, fifteen demonstrated particularly good expression levels in breast tumor over normal human tissues. The following eleven clones did not show any significant homology to any known genes. Clone 19463.1 (SEQ ID NO: 185) was over-expressed in the majority of breast tumors and also in the SCID breast tumors tested (refer to Example 2); additionally, over-expression was found in a majority of normal breast tissues. Clone 19483.1 (SEQ ID NO: 216) was over-expressed in a few breast tumors, with no over-expression in any normal tissues tested. Clone 19470.1 (SEQ ID NO: 219) was found to be slightly over-expressed in some breast tumors. Clone 19468.1 (SEQ ID NO: 222) was found to be slightly over-expressed in the majority of breast tumors tested. Clone 19505.1 (SEQ ID NO: 226) was found to be slightly over-expressed in 50% of breast tumors, as well as in SCID tumor tissues, with some degree of over-expression found in normal breast. Clone 1509.1 (SEQ ID NO: 232) was found to be over-expressed in very few breast tumors, but with a certain degree of over-expression in metastatic breast tumor tissues, as well as no significant over-expression found in normal tissues. Clone 19513.1 (SEQ ID NO: 236) was shown to be slightly over-expressed in few breast

tumors, with no significant over-expression levels found in normal tissues. Clone 19575.1 (SEQ ID NO: 240) showed low level over-expression in some breast tumors and also in normal breast. Clone 19560.1 (SEQ ID NO: 241) was over-expressed in 50% of breast tumors tested, as well as in some normal breast tissues. Clone 19583.1 (SEQ ID NO: 245) was slightly over-expressed in some breast tumors, with very low levels of over-expression found in normal tissues. Clone 19587.1 (SEQ ID NO: 246) showed low level over-expression in some breast tumors and no significant over-expression in normal tissues.

Clone 19520.1 (SEQ ID NO: 233), showing homology to clone 102D24 on chromosome 11q13.31, was found to be over-expressed in breast tumors and in SCID tumors. Clone 19517.1 (SEQ ID NO: 237), showing homology to human PAC 128M19 clone, was found to be slightly over-expressed in the majority of breast tumors tested. Clone 19392.2 (SEQ ID NO: 247), showing homology to human chromosome 17, was shown to be over-expressed in 50% of breast tumors tested. Clone 19399.2 (SEQ ID NO: 250), showing homology to human Xp22 BAC GSHB-184P14, was shown to be slightly over-expressed in a limited number of breast tumors tested.

In subsequent studies, 64 individual clones were isolated from a subtracted cDNA library containing cDNA from a pool of breast tumors subtracted with cDNA from five normal tissues (brain, liver, PBMC, pancreas and normal breast). The subtracted cDNA library was prepared as described above with the following modification. A combination of five six-base cutters (MluI, MscI, PvuII, SalI and StuI) was used to digest the cDNA instead of RsaI. This resulted in an increase in the average insert size from 300 bp to 600 bp. The 64 isolated clones were colony PCR amplified and their mRNA expression levels in breast tumor tissue, normal breast and various other normal tissues were examined by microarray technology as described above. The determined cDNA sequences of 11 clones which were found to be over-expressed in breast tumor tissue are provided in SEQ ID NO: 405-415. Comparison of these sequences to those in the public database, as outlined above, revealed homologies between the sequences of SEQ ID NO: 408, 411, 413 and 414 and previously isolated ESTs. The sequences of SEQ ID NO: 405-407, 409, 410, 412 and 415 were found to show some homology to previously identified sequences.

In further studies, a subtracted cDNA library was prepared from cDNA from metastatic breast tumors subtracted with a pool of cDNA from five normal tissues (breast, brain, lung, pancreas and PBMC) using the PCR-subtraction protocol of Clontech, described above. The determined cDNA sequences of 90 clones isolated from this library are provided in SEQ ID NO: 315-404. Comparison of these sequences with those in the public database, as described above, revealed no significant homologies to the sequence of SEQ ID NO: 366. The sequences of SEQ ID NO: 320-324, 342, 353, 367, 368, 377, 382, 385, 389, 395, 397 and 400 were found to show some homology to previously isolated ESTs. The remaining sequences were found to show homology to previously identified gene sequences.

In yet further studies, a subtracted cDNA library (referred to as 2BT) was prepared from cDNA from breast tumors subtracted with a pool of cDNA from six normal tissues (liver, brain, stomach, small intestine, kidney and heart) using the PCR-subtraction protocol of Clontech, described above. cDNA clones isolated from this subtraction were subjected to DNA microarray analysis as described above and the resulting data subjected to four modified Gemtools analyses. The first analysis compared 28 breast tumors with 28 non-breast normal tissues. A mean over-expression of at least 2.1 fold was used as a selection cut-off. The second analysis compared 6 metastatic breast tumors with 29 non-breast normal tissues. A mean over-expression of at least 2.5 fold was used as a cut-off. The third and fourth analyses compared 2 early SCID mouse-passaged with 2 late SCID mouse-passaged tumors. A mean over-expression in the early or late passaged tumors of 2.0 fold or greater was used as a cut-off. In addition, a visual analysis was performed on the microarray data for the 2BT clones. The determined cDNA sequences of 13 clones identified in the visual analysis are provided in SEQ ID NO: 427-439. The determined cDNA sequences of 22 clones identified using the modified Gemtools analysis are provided in SEQ ID NO: 440-462, wherein SEQ ID NO: 453 and 454 represent two partial, non-overlapping, sequences of the same clone.

Comparison of the clone sequences of SEQ ID NO: 436 and 437 (referred to as 263G6 and 262B2) with those in the public databases, as described above, revealed no significant homologies to previously identified sequences. The sequences of SEQ ID NO: 427, 429, 431, 435, 438, 441, 443, 444, 445, 446, 450, 453 and 454 (referred to as

266B4, 266G3, 264B4, 263G1, 262B6, 2BT2-34, 2BT1-77, 2BT1-62, 2BT1-60,61, 2BT1-59, 2BT1-52 and 2BT1-40, respectively) showed some homology to previously isolated expressed sequences tags (ESTs). The sequences of SEQ ID NO: 428, 430, 432, 433, 434, 439, 440, 442, 447, 448, 449, 451, 452 and 455-462 (referred to as clones 22892, 22890, 22883, 22882, 22880, 22869, 21374, 21349, 21093, 21091, 21089, 21085, 21084, 21063, 21062, 21060, 21053, 21050, 21036, 21037 and 21048, respectively), showed some homology to gene sequences previously identified in humans.

Example 2

ISOLATION AND CHARACTERIZATION OF BREAST TUMOR POLYPEPTIDES OBTAINED BY PCR-BASED SUBTRACTION USING SCID-PASSAGED TUMOR RNA

Human breast tumor antigens were obtained by PCR-based subtraction using SCID mouse passaged breast tumor RNA as follows. Human breast tumor was implanted in SCID mice and harvested on the first or sixth serial passage, as described in Patent Application Serial No. 08/556,659 filed 11/13/95, U.S. Patent No._____. Genes found to be differentially expressed between early and late passage SCID tumor may be stage specific and therefore useful in therapeutic and diagnostic applications. Total RNA was prepared from snap frozen SCID passaged human breast tumor from both the first and sixth passage.

PCR-based subtraction was performed essentially as described above. In the first subtraction (referred to as T9), RNA from first passage tumor was subtracted from sixth passage tumor RNA to identify more aggressive, later passage-specific antigens. Of the 64 clones isolated and sequenced from this subtraction, no significant homologies were found to 30 of these clones, hereinafter referred to as: 13053, 13057, 13059, 13065, 13067, 13068, 13071-13073, 13075, 13078, 13079, 13081, 13082, 13092, 13097, 13101, 13102, 13131, 13133, 13119, 13135, 13139, 13140, 13146-13149, and 13151, with the exception of some previously identified expressed sequence tags (ESTs). The determined cDNA sequences for these clones are provided in SEQ ID NO: 88-116,

respectively. The isolated cDNA sequences of SEQ ID NO: 117-140 showed homology to known genes.

In a second PCR-based subtraction, RNA from sixth passage tumor was subtracted from first passage tumor RNA to identify antigens down-regulated over multiple passages. Of the 36 clones isolated and sequenced, no significant homologies were found to nineteen of these clones, hereinafter referred to as: 14376, 14377, 14383, 14384, 14387, 14392, 14394, 14398, 14401, 14402, 14405, 14409, 14412, 14414-14416, 14419, 14426, and 14427, with the exception of some previously identified expressed sequence tags (ESTs). The determined cDNA sequences for these clones are provided in SEQ ID NO: 141-159, respectively. The isolated cDNA sequences of SEQ ID NO: 160-174 were found to show homology to previously known genes.

Further analysis of human breast tumor antigens through PCR-based subtraction using first and sixth passage SCID tumor RNA was performed. Sixty three clones were found to be differentially expressed by a two or more fold margin, as determined by microarray analysis, i.e., higher expression in early passage tumor over late passage tumor, or vice versa.. Seventeen of these clones showed no significant homology to any known genes, although some degree of homology with previously identified expressed sequence tags (ESTs) was found, hereinafter referred to as 20266, 20270, 20274, 20276, 20277, 20280, 20281, 20294, 20303, 20310, 20336, 20341, 20941, 20954, 20961, 20965 and 20975 (SEQ ID NO: 252-268, respectively). The remaining clones were found to share some degree of homology to known genes, which are identified in the Brief Description of the Drawings and Sequence Identifiers section above, hereinafter referred to as 20261, 20262, 20265, 20267, 20268, 20271, 20272, 20273, 20278, 20279, 20293, 20300, 20305, 20306, 20307, 20313, 20317, 20318, 20320, 20321, 20322, 20326, 20333, 20335, 20337, 20338, 20340, 20938, 20939, 20940, 20942, 20943, 20944, 20946, 20947, 20948, 20949, 20950, 20951, 20952, 20957, 20959, 20966, 20976, 20977 and 20978. The determined cDNA sequences for these clones are provided in SEQ ID NO: 269-313, respectively.

The clones 20310, 20281, 20262, 20280, 20303, 20336, 20270, 20341, 20326 and 20977 (also referred to as B820P, B821P, B822P, B823P, B824P, B825P, B826P, B827P, B828P and B829P, respectively) were selected for further analysis based

on the results obtained with microarray analysis. Specifically, microarray data analysis indicated at least two- to three-fold overexpression of these clones in breast tumor RNA compared to normal tissues tested. Subsequent studies led to the determination of the complete insert sequence for the clones B820P, B821P, B822P, B823P, B824P, B825P, B826P, B827P, B828P and B829P. These extended cDNA sequences are provided in SEQ ID NO: 416-426, respectively.

Example 3
SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on an Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

Claims

1. An isolated polypeptide comprising at least an immunogenic portion of a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (a) sequences recited in SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468;
- (b) sequences that hybridize to a sequence of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 under moderately stringent conditions; and
- (c) a complement of a sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 176, 179, 181 and 469-473.

4. An isolated polynucleotide encoding at least 15 contiguous amino acid residues of a breast tumor protein, or a variant thereof that differs in one or more substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a breast tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468.

7. An isolated polynucleotide comprising a sequence that hybridizes to a sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219,

222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 under moderately stringent conditions.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims claim 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with an immunostimulant.

15. A vaccine according to claim 14, wherein the immunostimulant is an adjuvant.

16. A vaccine according to claim 14, wherein the immunostimulant induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with an immunostimulant.

19. A vaccine according to claim 18, wherein the immunostimulant is an adjuvant.

20. A vaccine according to claim 18, wherein the immunostimulant induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a breast tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with an immunostimulant.

26. A vaccine according to claim 25, wherein the immunostimulant is an adjuvant.

27. A vaccine according to claim 25, wherein the immunostimulant induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-binding fragment thereof according to claim 21, and thereby inhibiting the development

of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is breast cancer .

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with an immunostimulant.

42. A vaccine according to claim 41, wherein the immunostimulant is an adjuvant.

43. A vaccine according to claim 41, wherein the immunostimulant induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with an immunostimulant.

46. A vaccine according to claim 45, wherein the immunostimulant is an adjuvant.

47. A vaccine according to claim 45, wherein the immunostimulant induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOS: 1-175, 178, 180 and 182-468; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the antigen from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.

52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a breast tumor protein, comprising contacting T cells with one or more of:

(i) a polypeptide according to claim 1;

(ii) a polynucleotide encoding such a polypeptide; and/or

(iii) an antigen presenting cell that expresses such a polypeptide;

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;
(ii) a polynucleotide encoding such a polypeptide; or
(iii) an antigen-presenting cell that expresses such a polypeptide;

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;
(ii) a polynucleotide encoding such a polypeptide; or
(iii) an antigen-presenting cell that expresses such a polypeptide;

such that T cells proliferate;

(b) cloning at least one proliferated cell; and

(c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

- (i) polynucleotides recited in any one of SEQ ID NOS: 1-175, 178, 180 and 182-468; and
- (ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is breast cancer.

62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 1-175, 178, 180 and 182-468 or a complement of any of the foregoing polynucleotides;
- (b) detecting in the sample an amount of polypeptide that binds to the binding agent;
- (c) repeating steps (a) and (b) using a biological sample obtained from

the patient at a subsequent point in time; and

(d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

63. A method according to claim 62, wherein the binding agent is an antibody.

64. A method according to claim 63, wherein the antibody is a monoclonal antibody.

65. A method according to claim 62, wherein the cancer is a breast cancer.

66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 1-175, 178, 180 and 182-468 or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

- (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 1-175, 178, 180 and 182-468 or a complement of any of the foregoing polynucleotides;
- (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;
- (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and
- (d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 21; and
- (b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

77. An oligonucleotide comprising 10 to 40 contiguous nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a breast tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468 or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 contiguous nucleotides recited in any one of SEQ ID NOS: 2, 4-15, 18-33, 35-47, 49-56, 58, 59, 63-73, 88-116, 141-159, 175, 178, 180, 185, 186, 194, 199, 205, 208, 211, 214-216, 219, 222, 226, 232, 236, 240, 241, 245, 246, 252-268, 320-324, 342, 353, 366-368, 377, 382, 385, 389, 395, 397, 400, 408, 411, 413, 414, 416, 417, 419-423, 426, 427, 429, 431, 435-438, 441, 443-446, 450, 453, 454 and 463-468.

79. A diagnostic kit, comprising:

(a) an oligonucleotide according to claim 77; and

(b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

SEQUENCE LISTING

<110> Corixa Corporation
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Mitcham, Jennifer L.
Xu, Jiangchun
Harlocker, Susan L.

<120> COMPOSITIONS FOR THE TREATMENT AND
DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

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35 40 45	
Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe Arg	
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Arg Asn Phe Pro Ile Pro Ile Pro Ser Ala Pro Thr Thr Pro Leu Pro	
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aaaaacagtg taaaaatcaca ctttgtctg taaacatatt tagcttgct tttcatttcag	240
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gcttcaatgg gaagagggtcc tgaacattca gctccattga atgtgaaata ccaacgctga	600
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gtgttcattt gaacccattt actgatctct gttgtatatt tttcatgccca ctgtttgtt	240

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aagtatagta aaatgtgac atctaaaact aaataaaatag aaaacaccag gccagaacta	660
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tccagaaaata tccgtacccca caaggacgta acagaaaatc tggagaccca agtggtagag	360
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<210> 67
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 <212> DNA
 <213> Homo sapien

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atattcccaa aaagaggctg agacaggagg ttatttcaa ttttatttttgaattaaata		360
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acacacatg aggacatcc ggttttgggt caatattgt a gacttttgg tggatgagat	480
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ccctttatg ggattgaaag cttt tttt accatggagaa atatattttt aat tttt gttat	660
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gtaagggaaag gaggaagacc ttgaggaatg ctggygatat tggyatcagc aatgcggatg      240
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<210> 74
<211> 401
<212> DNA
<213> Homo sapien

<400> 74
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ggtccacacaga gcactcatct ggctggctt tgggtgggtt ggctctactc aagaagcaaa      180
gcagttacca gcacattcaa acagtgttattt gaacatctt taaatatcaa atgtgagaaac      240
aagaaggcaaa cataataatg ttatcagaaa gatgttagga agtaaggaca gctgtgtaaa      300
gcttgaggctt gaaaagttagc ttggccagctt catttcttgc gtttcttggg tagtggggccg      360
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<210> 75
<211> 612
<212> DNA
<213> Homo sapien

<400> 75
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<210> 76
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<212> DNA
<213> Homo sapien

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<400> 76

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<210> 77

<211> 314

<212> DNA

<213> Homo sapien

<400> 77

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<211> 548

<212> DNA

<213> Homo sapien

<400> 78

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<210> 79

<211> 646

<212> DNA

<213> Homo sapien

<400> 79

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ctatgatatc	aatgaatgtg	gtttaagttaa	tagatttcca	gctaaattgg	tctaaaaaaag	180

aatattaagt	gtggacagac	ctatttcaaa	ggagcttaat	tgatctca	tgttttagtt	240
ctgatccagg	gagatcaccc	ctctaattat	ttctgaactt	ggtaataaaa	agtttataaag	300
attttatga	agcagccact	gtatgatatt	ttaagcaaat	atgttattta	aaatattgat	360
ccttccttg	gaccaccc	atgttagttg	ggtattataa	ataagagata	caaccatgaa	420
tatattatgt	ttatacaaaa	tcaatctgaa	cacaattcat	aaagattct	cttttataacc	480
ttcctcactg	gccccctcca	cctgcccata	gtcaccaaat	tctgttttaa	atcaatgacc	540
taagatcaac	aatgaagtt	tttataaaatg	tatTTatgt	gttagactgt	gggtcaaatg	600
tttccatTTT	caaattatTT	agaattctta	tgagttaaa	atttgtaaat	ttctaaatcc	660
aatcatgtaa	aatgaaactg	ttgcgtccatt	ggagtagtct	cccacctaaa	tatcaagatg	720
gctatatgt	aaaaagagaa	aatatggtca	agtctaaaat	ggctaattgt	cctatgtatgc	780
tattatcata	gactaatgac	atttatcttc	aaaacaccaa	attgtctta	gaaaaattaa	840
tgtgattaca	ggtagagaac	ctcgcccg	accacgct			878
<210>	83					
<211>	645					
<212>	DNA					
<213>	Homo sapien					
<400>	83					
acaaacattt	tacaaaaaaag	aacattacca	atatcagtgg	cagtaaggc	aagctgaaga	60
ataaaatagac	tgagtttccg	ggcaatgtct	gtcctcaaaag	acatccaaac	tgcgttcagg	120
cagctgaaac	aggcttcttt	cccagtgcaca	agcatatgtg	gtcagtaata	caaacgatgg	180
taaatgaggc	tactacatag	gcccaagttaa	caaactcc	ttctccctcg	gtaggccatg	240
atacaagtgg	aactcatcaa	ataatTTaaa	cccaaggcga	taacaacgct	atttcccattc	300
taaactcatt	taagccttca	caatgtcgca	atggattcag	ttacttgcaa	acgatcccgg	360
gttgtcatac	agatacttgt	ttttacacat	aacgctgtgc	catcccttcc	ttcaactgccc	420
cagttaggtt	tcctgttgtt	ggaccgaaag	gggatacatt	ttagaaatgc	ttccctcaag	480
acagaagtga	gaaagaaagg	agaccctgag	gccaggatct	attaaacctg	gtgtgtgcgc	540
aaaagggagg	gggaaggcag	gaatttgaaa	ggataaaacgt	ctcctttgcg	ccgaggaatc	600
aggaagcgtg	actcacttgg	gtctgggacg	ataccgaaat	ccgg		645
<210>	84					
<211>	301					
<212>	DNA					
<213>	Homo sapien					
<220>						
<221>	misc_feature					
<222>	(1)...(301)					
<223>	n = A,T,C or G					
<400>	84					
tctgatgtca	atcacaactt	gaaggatgcc	aatgtatgtac	caatccaatg	tgaaatctct	60
cctcttatct	cctatgtgg	agaaggatta	gaaggttatg	tggcagataa	agaattccat	120
gcacctctaa	tcatcgatga	gaatggagtt	catgggctgg	tgaaaaatgg	tatTTgaacc	180
agataccaag	ttttgttgc	cacgatagga	atagctttta	ttttgatag	accaactgtg	240
aacctacaag	acgtcttgg	caactgaagn	ttaaatatcc	acangggtt	attttgcttg	300
g						301
<210>	85					
<211>	296					
<212>	DNA					
<213>	Homo sapien					
<220>						

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<221> misc_feature
<222> (1)...(296)
<223> n = A,T,C or G

<400> 85
agcgtgggtc gcggcncgan gtagagaacc gactgaaacg tttgagatga agaaaagttct      60
ccttcgtatc acagccatct tggcagtggc tggtggttt ccagtctctc aagaccaggaa     120
acgagaaaaaa agaagtatca gtgacagcga tgaatttagct tcagggtttt ttgtgttccc     180
ttaccccatat ccatttcgcc cacttccacc aattccattt ccaagatttc catggtttan     240
acgtaatttt cctattccaa tacctaatac tgccccatac actcccccttc cttagcg      296

<210> 86
<211> 806
<212> DNA
<213> Homo sapien

<400> 86
tctacgtgg ccatttgctc attgtctttc ctctgtgtgt agtgagtgc cctggcagtg      60
tttgcctgct cagagtggcc cctcagaaca acagggtgg ccttggaaaa accccaaaac     120
aggactgtgg tgacaactct ggtcaggtgt gatttgacat gagggccgga ggcgggttgc     180
gacggcagga ctggagaggc tgcgtgcccgc gcaactggcag cgaggctcgt gtgtccccca   240
ggcagatctg ggcacttcc caaccaggat ttatgccgtc tccaggaaag cctcgggtgcc   300
agagtgggtgg gcagatctga ccatccccac agaccagaaa caaggaattt ctgggattac   360
ccagtcccccc ttcaacccagg ttgatgtAAC cacctcattt tttacaaata cagaatctat  420
tctactcagg ctatgggcct cgtccctcaact cagttattgc gagtggttgc gtccgcattgc 480
tccggggcccc acgtggctcc tgtgtcttag atcatggtga ctcccccggcc ctgtgggtgg 540
aatcgatgcc acggattgca ggccaaattt cagatcgtgt ttccaaacac ccttgcgtgtg 600
ccctttaatg ggattgaaag cacttttacc acatggagaa atatatttt aatttgttat 660
gctttctac aagggtccact atttctgagt ttaatgtgtt tccaacactt aaggagactc 720
taatgaaagc tgatgaattt tctttctgt ccaaacaagt aaaataaaaaa taaaagtcta 780
tttagatgtt gaaaaaaaaaaaaaa 806

<210> 87
<211> 620
<212> DNA
<213> Homo sapien

<400> 87
tttttgcattc agatctgaaa tgtctgagag taatagtttc tggtgaattt tttttgttc      60
atttttctgc acagtccatt ctgtttttat tactatctag gcttggaaaata tatagtttga 120
aatttatgaca tccttcctct ttgttatttt cctcatgatt gctttggcta ttcaagttt 180
attttagttt catgttaattt ttgttattgtt attttccattt attgtaaaaa tagtaccact 240
gcaattttaa taggaaggattt attgaatcta tagattactt tggataatat ggcacttcaa 300
taatattcat gttttcaattt catagacaaa atatttaaa atttattttgtt atctttctat 360
atttttctt tttttatgtt aaagattttac ctccctgggtt aatatttcc tcagaaattt 420
attattnaag gtatagtcac taaaattttc ttcccttattt ttgtcagata gtttaagtgt 480
atgaaaccat agatataactt gtatgttattt gctaattttac tgagtgtattt 540
tatttagttt gagaggtttt aatgtactgt ttatggttt taaaatataa gattacttat 600
tttttaaaaaa aaaaaaaaaaaa 620

<210> 88
<211> 308
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(308)
<223> n = A,T,C or G

<400> 88
tagctgtgnt cagcagggcc aggtttttt ttttttttag atggagtctc gccctgtcac      60
ccaggctgga gtgcagtggc ctgatctcag ctcactgaa gctccacctc ctggattcac      120
gtatttcctcc tgccctcagcc tcccaagtag ctgggactac aggccccgc caccacgccc      180
agctaattnt ttgnattttt agtacnagat gcgggttcat cgttttagcc agcatggnct      240
cgatctccctg acctcgtgaa ctgcccgcct cggccctccca aagacctgcc cgggcnggcc      300
gctcgaaa      308

<210> 89
<211> 492
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(492)
<223> n = A,T,C or G

<400> 89
agcggcccgcc cgggcaggc tggtaagtaa catacatatc accttaataa aaatcaagat      60
gaaatgtttt agaaactatt ttatcaaaag tggctctgat acaaagactt gtacatgatt      120
gttcacagca gcactattaa tgccaaaaag tagacaaaac ctaaatgtcc attaactgat      180
aagcaaaatg tggtatatcc atacaatgga atattatgta gcccacaaca tggcatggag      240
tactacaaca tggatgagcc tcaaaaacgt tatgctaat gaaaaaagtc agatataggaa      300
aaccacatgt catatgatcc catttatatg aaatagccag aaaaggcaag tcataaaaaac      360
aagatagatc ggaaaaatggg ttggaggact acaaatggca ccagggatct ttgaagttga      420
tgaaaaatggt ctaaaatccag actgtggntg tggtaaca agtctgtaaa ttaccaaaaa      480
tgcgttaata ca      492

<210> 90
<211> 390
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(390)
<223> n = A,T,C or G

<400> 90
tcgagcggcc gcccgggcag gtacaagctt tttttttttt tttttttttt ttttctaaca      60
gttctctgtt ttattgcaat acagcaaagt ctggtaataa ttaangata tcaacataaaa      120
gtattggtga ggagtctttt gtgacattttt ttaccatccc accttaaataa tttctgtgca      180
aaanaatcca catcattgtt tggtancana ggatctcta aaaagttccc taanacactg      240
agggcataaaa accaaacaaa ataaaaataag gagtgatagg ctaaagcagt atcttccct      300
ccatccacat ttgncaagca ttatattcta accaaaaat gatcacacca ggcctatgcaa      360
aactgtccaa tattaccgag aaaaaacccct      390

<210> 91
<211> 192

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<212> DNA
 <213> Homo sapien

<400> 91
 agcgtggtcg cggccgaggt ctgtcaarta atgcttagtcc tcaggattta aaaaataatc 60
 ttaactcaaa gtccaatgca aaaacattaa gttggtaatt actcttgatc ttgaattact 120
 tccgttacga aagtcccaa cattttcaa actaagctac tatatttaag gcctgcccgg 180
 gcggccgctc ga 192

<210> 92
 <211> 570
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(570)
 <223> n = A,T,C or G

<400> 92
 agcgtggtcg cggccgaggt ctgacaacta acaaagaagc aaaaactggc atcttgaca 60
 tcctagtatt acacttgc当地 gcaatttagaa cacaaggagg gccaaaggaaa aagtttagct 120
 ttgaatcact tccaaatcta ctgatttga gggtccgc当地 tagttctaac aaaaactttc 180
 agacaatgtt aactttcgat taagaaagaa aaaaacccca aacatcttca ggaattccat 240
 gccaggttca gtctcttcca gtgagccgc当地 ttgctaaaag tccacgtgca ccattaattt 300
 gctgggctgg cagcacatg taaaaagaag cctattcacc accaaccaca cagactagac 360
 atgtaaaatgta ggatcaagta atggatgaca accatggtcg tgaaatatgg tcaatgagag 420
 tcagaaaatgta acaggcacca gtacaaggc当地 cagataacag aattgacggg ccaaaggata 480
 aaaataggct tatttaataa ggatgctaca gaacacatnc acttcttaatt ggaagctgct 540
 ttacactggg tggcattgna ccatatgcat 570

<210> 93
 <211> 446
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(446)
 <223> n = A,T,C or G

<400> 93
 tcgagcggcc gccccggc当地 gtccagggtt ttatTTAGT gtgtaatctt ggacaagtta 60
 cctaactttt ttgagttctga atatattaa tctgaaaaat gagaatcatg ataatacgatc 120
 ataggcttaa ttaggaggat taaatgaaaat aattttatagg tgggccatg gttacataca 180
 agtatttagta gttaattctt ttcccttggt tactttataa gtatagggtt gatgaagggt 240
 ccagtatagg caaaaataact acttgggggt aaagtagagt gtgataactt atttggaaatg 300
 ttccctgaat ctgatcttta ctttttgnta ctgctgc当地 accaaaatcc aaattttcat 360
 cccaaacatttcc ttggatttgtt gggacagcng tagcagctt tccaaatataa tctataactac 420
 atctttctt actttggtgc tttttg 446

<210> 94
 <211> 409
 <212> DNA
 <213> Homo sapien

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<400> 94
cgagcggccg cccgggcagg tccatcagct cttctgctta gaatacgagg cagacagtgg      60
agaggtcaca tcagttatcg tctatcaggg tgatgaccca agaaaggta gtagagaaggt      120
gtcggcacac acgcctctgg atccacccat gcgagaagcc ctcaagttgc gtatccagga      180
ggagattgca aagcgcaga gccaacactg accatgttga aggcttctc tccaggctgg      240
attcaactgca ctcggaaagaa ttctgcccag ggaatttagt gtgggggtac caggaccagt      300
ttgtcttgat cttgagaccc ccagagctgc tgcatccata gggtgttgc ggactacacc      360
tggcctgcct tgcagtcatt ctttcttata ttttgaccca tttgccccaa                  409

<210> 95
<211> 490
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(490)
<223> n = A,T,C or G

<400> 95
tcgagcggcc gcccgggcag gtctacttg tttgcagctt ccacacactg cacctaccta      60
ctacctcttcttccatgctta actgggttta gaaagggttag ctatgcgttag aagaactact      120
tggatattt aagtgtgtt tttgaacgt aaggctatacg ataacagtct gaagctgcaa      180
gggagacttt gttgttacac tactataaac aggttaaacta cctgtttgtt cttgtatatag      240
tgcataatgaa atgactgtt taataaaaaa ctacagaaca tgcaaaaattt tttctgagat      300
gttaagtatt acttcagtgg agaacaaaaac ttacttaacc tttcgctaat gcatgttagta      360
ccagaaagca aacatggttt tagttccctt tactaaaaat atgaacattt agtgggttgt      420
aattttgtct gccaagtggt tcagaaaaata cattataaaat aacctaagtt aaaaaaaaaaaga      480
aactgngaac                                490

<210> 96
<211> 223
<212> DNA
<213> Homo sapien

<400> 96
agcgtggcgtcg cggccgaggt ctggaaagccc accctaggac ttgaatggca cttgtccctt      60
tctctgccag taatgcaatc caacacaata tgctacaggg aaaacagaat ttccacggtg      120
ccgcctctg gtacaaggga aacacgcacgc aaagcaaaag gccacagagg gctccctgag      180
aatccagtagac aactaagcga ggacctgccc gggcggccgc tcg                                223

<210> 97
<211> 527
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(527)
<223> n = A,T,C or G

<400> 97
tcgagcggcc gcccgggcag gtctgtgcag gagacactga agtgggttagt gtccataatc      60
tttttagcct gttgctgaaa ttccagttgt actccttcaa accaaaaatgc ttacaggatc      120

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atgggaaaagc	ctcggttgca	gaaatcaaga	caggcaagtg	ggaagataac	tcggcttga	180
ggttaaacag	atctgggttc	aaagcatagt	ttcaactct	gtcttgtaa	gtgtcctggg	240
tgaagtcat	tcctctttg	aatttcagag	aggataaaaa	tataaaaagt	ataataacta	300
tcttcataat	ctttgtgagg	attnaagaag	acgaagtgtg	tgaaaagcta	agcacagagc	360
aggcattcta	caataagtag	ttattatTTT	tggAACCATC	ccgnccctag	ccccagcccc	420
attaccttct	cttagnctct	tcatatcgaa	ngccgtaaatc	ttgaccttct	ottgcnaactg	480
gattggtgct	ggttgatgcc	caaacttccc	gagatgtgt	ctggaa		527
<210>	98					
<211>	514					
<212>	DNA					
<213>	Homo sapien					
<220>						
<221>	misc_feature					
<222>	(1) ... (514)					
<223>	n = A,T,C or G					
<400>	98					
tcgagcggcc	gcccgggcag	gtctggctcc	catggccctt	ggggtggcct	gactctgtca	60
ctattcctaa	aaccttcttag	gacatctgt	ccaggaagaa	cttcaacac	caaaattcat	120
ctcaatttta	cagatggaa	aagtgtattct	gagaccagac	cagggtcagg	ccaagggtcat	180
ccagcatca	tggctggct	gagactgggc	ccagggaaacc	ctgtctgtctc	ctctttttcc	240
cagagctgt	agttctctag	ccaaggctgc	actcttgagg	gagagccagg	aagcatagct	300
gaggccatga	caacctca	cttcacactga	aaatTTAACC	cgtggcagag	gatccaggca	360
catataggct	tcggagccaa	acaggacctc	ggccgcgacc	acgctaagcc	gaattccagc	420
acactggcgg	ccgttactag	tggatcccga	gcttnggtac	caagcttggc	gtaatcatgg	480
gcatacgctgg	ttcctggggt	gaaaatggta	tccg			514
<210>	99					
<211>	530					
<212>	DNA					
<213>	Homo sapien					
<220>						
<221>	misc_feature					
<222>	(1) ... (530)					
<223>	n = A,T,C or G					
<400>	99					
tcgagcggcc	gcccgggcag	gtctgaagaa	acaggtataa	atttggcagc	cagtaatttt	60
gacagggaaag	ttacagcttg	catgacttta	aatatgtaaa	tttggaaaata	ctgaattttcg	120
agtaatcatt	gtgctttgt	ttgatctgaa	aaatataaca	ctggctgtcg	aagaagcatg	180
ttcaaaaata	tttaattcac	ttcaaaatgt	catacaaatt	atgggtgttt	ctatgcaccc	240
ctaaagcttc	aagtcattha	gctcaggta	atactaaagt	aatatattaa	ttcttccagt	300
acagtggtgt	ttcataccat	tgacatttgc	ataccctaga	ataatTTAAG	aaagacatgt	360
gtaatattca	caatgttcag	aaaagcaagc	aaaaggtaaa	ggaacctgct	ttggttcttc	420
tggagatggn	ctcatatcag	tttcataaaac	attcattcta	aaaaatagta	agctaaccat	480
ttgaacccca	atttccagat	taagcatatt	ttctcataaaa	tnatgaagcc		530
<210>	100					
<211>	529					
<212>	DNA					
<213>	Homo sapien					

<400> 100	
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gaggctgagg gaggtggatc acttgagtcc aggagtttga gaccagtctg gccaacatgg	120
cggaaacttca tcactaccaa agaagaaaaa aatttagccag gtgtgggt gtatgcctgt	180
agtcccagat actctggtgg ctgaggtgag aggatacgctt gagccagga aattgaggct	240
gcagtgaact atgattgcac tactgtgctc cagcttggc aacagagtga gatcttgtct	300
ccaaaagtcc ttgaaggatt ttaggaagtt gttaaaagtc ttgaaacgat gtttggggc	360
atgttagggt tcttgaatgt ttaattcctc taataactgc ttattcaaga gaagcatttc	420
tgaactgggtg cggggcagtg gcttcatgcc ccataatccc agtacttgg gaggctgaag	480
caggaacatt gcttgagccc aggactcaa gaacagcctg ggtaacata	529
<210> 101	
<211> 277	
<212> DNA	
<213> Homo sapien	
<400> 101	
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gagggAACGA gatcttgagc tgaaaatggg agatgattat attttggatc ttcaagatc	120
ctgggattta atgaatttgt ctggaaaaca tgataagata ccagaaaatct gggaggc	180
taatatagct gattatattt atccagccat catgaagaaa ttggaagaat tagaaaaaga	240
agaagagctg agaacagacc tcggccgcga ccacgct	277
<210> 102	
<211> 490	
<212> DNA	
<213> Homo sapien	
<400> 102	
gcgtggtcgc ggccgagggtc tgacggcttt gctgtcccag agccgcctaa acgcaagaaa	60
agtgcgtggg acagtttagag gggatgtgct aaagcgtgaa atcagttgtc cttatTTT	120
agaaagattt tggtaacttag gtgtctcagg gctgggtgg ggtccaaagt gtaaggaccc	180
cctgccccta gtggagagct ggagcttggaa gacattaccc cttcatcaga aggaattttc	240
ggatgttttc ttgggaagct gttttggtcc ttggaagcag tgagagctgg gaagcttctt	300
ttggctctag gtgagttgtc atgtggtaa gttgagggtt tcttggata aagggtcttc	360
tagggcacaa aactcaact aggtttatata tttatgttagc ttatTTTT tactaagggtg	420
tcaacctata agcatctata aattgacttc tttttcttag ttgtatgacc tgccccgggc	480
ggccgctcga	490
<210> 103	
<211> 490	
<212> DNA	
<213> Homo sapien	
<400> 103	
gagcggccgc cggggcagggt ccaaaccagc ttgctataa gtcattaacc aaatccatta	60
taggttaattt gttcaggta atgtttacaa ttcttatgga aaaaattagc aacacacaca	120
tttAAACGT gtgcattttac ctttgcgtga gtgcctaaaa tacatatttc tatttcaaga	180
tgacatttaa aaattattct aatatatcg cagcaaaaataatgtca attacaaaaa	240
actaaaactag aatccttaag ttattctcat gtttacagggt gtgattctt aataaaataact	300
attatgcagc tctattgttt aagctttctg gatttggttt aaacacatgc atatataattg	360
tcaattgtgg gaagctttac aagttatatt ccatgcactt tttggacaga gttctaacag	420
agccagccag tccacaaaac aggcaagaca aaagttgaat taactggggc aaaataggac	480
tcttatgcaa	490

<210> 104
 <211> 489
 <212> DNA
 <213> Homo sapien

<400> 104
 cgtggtcgctg gcccgggtcc aggctggtct cgaactcctg accttgtat ctggccgcct 60
 cgccctccca aagtgttggg attacaggca tgagccactg cgcccgaccg agttgaacat 120
 ttaatgttag actaggccag agttgttcaa tctttttattt ctcacttcccc aaaggagccg 180
 ttggagattt tccccctcaat ctctctccctt catggaaattt cataccacaa atatagtatg 240
 ttttattttat gtactgtgac ccttggaaagg atcacaaaacc aatataatag tttttttttt 300
 taaccctgtca aggaccaagt ttttggccctt gttggaaatg cataaaactgg actgtatgaat 360
 tggatagat ggcttttatac atgaggatca gaaaaacttg aaatttccctt gctacgacac 420
 tcacatattta tcaccgtata gggaggacct tggatggggg aagttagaaac actttctacac 480
 ttacagca 489

<210> 105
 <211> 479
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 105
 gcgtggtcgc ggccggaggc tgactggctt cagccccaga agttgagctg gccttttagac 60
 aaaataattt cacccctccctc tgctgttat tcccttcgggtttcatggg agtgtgaaca 120
 gttagataaa atctgtggct gncttccca ccttgctcta gtttccattt ctgtgagcag 180
 gccctccctat gccccggatt tagctacaat gctgtggact cacttgattt tttttctccg 240
 agttttgtct agaaatatgt gaaggtgagg ttaagtgtt ctctgtgttag atccacttag 300
 ccctgtctgc tggatgttgc ggcgttgctt cgtctctccctt ctcttccatc ctttccat 360
 gcttctccacc accttctggc ttcttttctt aatgcaataa aggcaatggg taacaaagaa 420
 agaatgtggg ctggaggtt agacagacct ggnntttaaat tctgtttctg gctctccaa 479

<210> 106
 <211> 511
 <212> DNA
 <213> Homo sapien

<400> 106
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 accgtccagc gattctagaa catttctgtt agggaaagaca tagcaaggaa ttttcatgtat 180
 tggggaaatac tgggagacaa gctgaagatt tggatgggc tatgtttctg tcatcttttta 240
 ggtatTTTaaag gctactccctt tagctagctt ctggagctg ttggaaatgtt ctatctccct 300
 acacagagtt acacaatgag catctctgaa agagaatatt accctggatt tccaaagatg 360
 tactctaaaca ggtgaccag gcaaaaggtt acccgggggg ggagttgtt ataacactcg 420
 gaccacatg ttctcaaggc acttcagaac ttggggaaat cattttgtac cggatcctca 480
 gaaagcattt atggaaatac acatccctta g 511

<210> 107
 <211> 451
 <212> DNA

<213> Homo sapien

<400> 107

ggccgcccgg gcaggtccag aatatcaaat caaaaggcataaaatgtca	cttcctcc	60
caccctctta catattggat cttaattgc aatagggagt gtaagatggg	catttttagag	120
acgttagttgc atcagcagaa gcaaaccat cttatacataaa tgggtttgg	ggataggaaa	180
aggctgctaa aaattcacaa gtcaccatc cccagaagca atgaatagcc	gtagaagacc	240
aaggaagatc aacaagttc caaagtgcata aagccagaga tttggccctt	ccaaaatacc	300
accaggacgc ctggaccctg gggctctccg catgtcacca ctgactgcca	ggatgctgct	360
gcacctccct tccttgagac acaacagaga gacagtgaag tcacccaaga	ctgggatcat	420
cagaggctcc tcatgctgc tacagagaag c		451

<210> 108

<211> 461

<212> DNA

<213> Homo sapien

<400> 108

ccgccccggc aggtcctgaa aacattcaga ctaatcaaaaa tggtactact	gtaaacttctt	60
ataatacata atataaaagt ttttggaaaga tatagacaca attaaccctt	aaacaacaca	120
ctatctgatt ctcaaaagca atggctattt aacaagatgt aaaaggacaa	taacatataca	180
aagaactttc acacacctaagatagcatt tagcagcaag tttagtcagac	aaaacaaaaca	240
caaataatttt cacatttctt atgtttgttt ttaactttac ttctataaagc	cactgataat	300
ttagggtttct ttcaagtata agatttctaa aattaaaaac tgtttttgac	atatttttat	360
aaagaaataaa aaagcaaaac gcaatccaac tatttataatg agtcccttctt	ctccaaacagc	420
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<210> 109

<211> 441

<212> DNA

<213> Homo sapien

<400> 109

ggccgcccgg gcaggtctga ttataagaga aagaaatcca gtgacacgag	ggcaggcagg	60
ccccgcctcg ctctgatcga gaaaagcttc ctgatgtcag ggagatggaa	ctgccaccat	120
cagaaccatg gcactttggg tgaagggtgtg tcagcgaacca agggggcagg	aaatgggcag	180
tgactaagggg ggcaggaaac aggccaggcac atggcaagggt tctccagcc	catcagccca	240
gtgatggcct cgattttggaa gctgcactac tgtctgaaaa gcacaattac	tggtgactct	300
taacaaacctt cagcatactg gggaggaga ctgtcaagta actgaattgg	aaagatgaaa	360
aagaaccatc tctaaaatgtt gatgcttgta agaagaataa cctcccttgt	gcaagtcttgc	420
caacatcttc attcaaccac a		441

<210> 110

<211> 451

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(451)

<223> n = A,T,C or G

<400> 110

ggtcggccggc gaggtctggg gaaggggtga gaatccctgg gccttgccca	gtcctgagct	60
ctgggtgtct gcaggaaagc acagtggtga gtttagtgtta aagaaagcat	ccagagaggt	120

aagaggggct tggtagcac ccttgccctc tgtcaactcc gaaaaactt cttgttgagg	180
aggaagatga gaaggtgac attgactttg gccttggta agagttcat gacagccaca	240
ccctcatact ggagctgcan gagatcctga tagtgaagct tgaaatcgct ccatgtccac	300
acccaggaac ttggcattt ctccaaactt tcctgcctca tctccggcg tgatgtcaaa	360
natgacgttt cttgaagtga gaggcggaa agatcttcaa tttccaccaa agacaccctt	420
tttccagga gctttagcaa caagtgtaat g	451
<210> 111	
<211> 407	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(407)	
<223> n = A,T,C or G	
<400> 111	
ggccgacgtt cgacctgact tcttngagc agntgncaact acccgctttg aggaatgccg	60
actgcagaca gtggccang gcaaagagtg tgcgtcatcg atganattgg naagatggag	120
ctcttcagtc agnntttcat tcaagctgnt cgtcagacgc tgcgttacccc agggactata	180
atccttngca caatcccaactt tcctanagga aagccactgn ctctttaga agaaatcana	240
cacanaaaagg atgtgaacng tggtaatgt caccaaggaa aaacatgaaa ccacccctg	300
ccagatatcg ggacgttgcg tgcagatcaa gcacgnaagt gaagacgcgt gcattccctg	360
ccttccgtga acgantgccc agntcaagaa ganctgatg gaaccct	407
<210> 112	
<211> 401	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(401)	
<223> n = A,T,C or G	
<400> 112	
tgcggccga ggtcgccga ggtctgacat ctgttgtctg tgataaccac ttctgtattt	60
cgtcttaacc acttctgtat tgggtggttt taactgccta aggccgcaat gggcagtggg	120
cccccttccc ttaggatggg tatcaattca acaatattta taaggcattt actgtgtgct	180
aagcatttgg aagaccagg ctacaaaata agacatagg cctgcctcc agggcagcag	240
agggaggcac aaataccagg gaatctctga tgggtgtgaa gtgcggcgt gggccacaga	300
aaatgaccgt catggagacc ctgtaaagg tcggaccctg agcccaaagg ggtattcaga	360
agnngagatg attttggccc cactcataga tgggtggcaa a	401
<210> 113	
<211> 451	
<212> DNA	
<213> Homo sapien	
<400> 113	
gtcgccggccg aggtccatat taaaaagtcc atcataaaca aagactcctc ctcatggtat	60
gaatatgctc catatgcca taatggtgca taacggacctt agaaattcca atgagtctta	120
gggttggaaat ttccaatgac ctgagcaagg cagctccctt tagcttctgg ataacatttt	180
acacccagag ttcaaggctt aacagaccta tcaacacaat tatttcgga ttgtctgtct	240

agaaaaacggc aatgctaaa ggaatataaa taagggtggg gggacatatg cttccagcct	300
ggccttctc catgtggtaa aaaacaatgg aatggctgt ttaattttt ttaatcttt	360
tctgacctt actatgttg gtaatggaaa taagtcaagg aaaacaaaat gaacaggct	420
catcaactaa ttaatactgg gtttcttct t	451
<210> 114	
<211> 441	
<212> DNA	
<213> Homo sapien	
<400> 114	
ggccgcccgg gcaggtccat cctgtcagag atggagaag tcacagacgg aatgatggat	60
acaaaagatgg ttcaacttct tacacactat gctgacaaga ttgaatctgt tcattttca	120
gaccagttct ctggtccaaa aattatgcaa gaggaaggtc agccttaaa gctacctgac	180
actaagagga cactgttgc tacatthaat gtgcctggct caggtAACAC ttacccaaag	240
gatatggagg cactgttacc cctgatgaac atggtgattt attctattga taaagccaaa	300
aagttccgac tcaacagaga aggcaaacaa aaagcagata agaaccgtgc ccgagtagaa	360
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ggaagaaaaa aagaacagag a	441
<210> 115	
<211> 431	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(431)	
<223> n = A,T,C or G	
<400> 115	
gccggccggg caggtccatt ggcggtgaca aaaggaaaaag aagcaaaagag actcagtccca	60
taatgctgat tagtttagaaag aaagggttag gattgagaaa gtaccaggaa ctttttaatta	120
ttttaaaagag aatgctgact gttaatgttt taaatcttac tggtccaaatg tactaatatg	180
aatttttacc ctttgtgcat gaatattcta aacaactaga agacccctccac aatttagcag	240
ttatgaaagt taaaactttt attataaaaaa ttctaaacct tactgctcct ttaccaggaa	300
catgacacac tattnancat cagttgcata cctcgccaaat agtataattc aactgtcttg	360
cccgaaacaat catctccatc tggaaagacgt aagcctttag aaacacattt ttctattaat	420
ttctctagaa c	431
<210> 116	
<211> 421	
<212> DNA	
<213> Homo sapien	
<400> 116	
gtcgccggccg aggtccagaa atgaagaaga agtttgacaga tgtatggca aagaagacga	60
aggcagagtg gtgtcaaatc tttgacggca cagatgcctg tgtgactccg gttctgactt	120
ttgaggaggt tggtcatcat gatcacaaca aggaaccggg gctcggttat caccagttag	180
gagcaggacg tgagcccccg ccctgcacccct ctgctgttaa acaccccagc catcccttct	240
ttcaaaaggg atcccttcat aggagaacac actgaggaga tacttgaaga atttggattc	300
agcccgcgaa gagatttatac aagcttaact cagataaaaat cattgaaagt aataaggtaa	360
aagctaaatgc tctaacttcc aggccccacgg ctcaagtgaa tttcgaatac tgcatttaca	420
g	421

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<210> 117
<211> 489
<212> DNA
<213> Homo sapien

<400> 117
agcgtggtcg cggccgaggtaaggctgcga ggttgggg tctgggaaac tccgaggaca      60
gagggtctaaa tccatgaagt ttgtggatgg cctgatgatc cacagcgag accctgttaa     120
ctactacgtt gacactgttg tgcccacgt gttgctcaga cagggtgtgc tgggcatcaa     180
ggtaagatc atgctgccct gggaccacac tggttaagatt ggccctaaga agcccctgcc     240
tgaccacgtt agcattgtgg aacccaaaga tgagatactg cccaccaccc ccatctcaga     300
acagaagggt gggaaagccag agccgcctgc catgccccag ccagtcacca cagcataaca     360
gggtctccctt ggcagacctg cccgggcggc cgctcgaaag cccgaattcc agcacactgg     420
cggccgttac tagtggatcc cagctcggtt ccaagcttgg cgtaatcatg gtcatagctg     480
gtttcctgtt      489

<210> 118
<211> 489
<212> DNA
<213> Homo sapien

<400> 118
tcgagcggcc gcccgggcag gtattgaata cagcaaaatt ctatatacaa agtgacactgg      60
acctgctgct tcaaaacatg atcccttctt actaatatct tgatagtcgg tccatagagc     120
attagaaagc aattgactct taaataaaca gaaaagtgcc taatgcacat taaaatgaatg     180
gcctaactac tggaaactta gtagttctat aaggtgatta acataggttag gatccagttc     240
ctatgacagg ctgctgaaga acagatatga gcatcaagag gccatttgt gcactgcccac     300
cgtgatgcca tcgtgtttctt ggatcataat gttccatata tctgattcta gacacaccac     360
agaatatca gtgggggtcag aggttagctt agctgcttgc tgggctagaa cagatatacactc   420
tccagcatgc tcatctgaca gggtcccgcg gcaacccaga ttaagtccctt gtgaatctgt     480
gcacaggga      489

<210> 119
<211> 181
<212> DNA
<213> Homo sapien

<400> 119
taggttccag agacttttgg cccaggagga atatttactt ttagctctgg acatcattac      60
aaaaaggaat atttccaaa cctcttcaga ccgagaatac atggtaaaa ttatataata     120
gttgtataat aaaaataatt ttttccttaa aaaaaaaaaa aacctcgcc gcgaccacgc     180
t      181

<210> 120
<211> 489
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(489)
<223> n = A,T,C or G

<400> 120
gcgtggtcgc ggccgaggtc cattaaaaac aaagaaaaat actaaagcca ctagtaaaca      60

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tctgatgtgc	aaaataacaac	atcctctagt	tggctttatg	ccattattac	ataagctcca	120
aatagctcat	cttaaattaa	aaagaaaaag	tggctgtccc	atctctgctg	cataaatcag	180
atttttttt	aaaggtttag	agtactttaa	ggaagggaag	ttcaaaaactg	ccagtgaaat	240
tcacagagaa	tacaaatttt	gcaatttaat	ttcccaaagc	tcttgaaga	agcaagagag	300
tctctttct	taatgcagt	ttctccaaag	aggaactgta	attttgcttg	gtacttatgc	360
tgggagat	gcaaaatgt	tttttcaatg	tttgctagaa	tataatggtt	cctttcagt	420
gnctggttca	tccttggaa	act catgggtt	aaaggacttc	ttggagccga	actgccccgg	480
cgggcccnn						489
<210>	121					
<211>	531					
<212>	DNA					
<213>	Homo sapien					
<400>	121					
cgagcggccg	cccgccagg	tggccagcgc	tggtccccga	gacgccgaga	tggagggaaat	60
atttgcgtat	gcgtcacctg	gaaagcaaaa	ggaaatccaa	gaaccagatc	ctaccttatga	120
agaaaaaaatg	caaactgacc	gggcaaatag	attcgagtt	ttattaaagc	agacagaact	180
tttgcacat	ttcattcaac	ctgtgtca	gaagactcca	acttcacctt	tgaagatgaa	240
accaggccgc	ccacgaataa	aaaaagatga	gaagcagaac	ttactatccg	ttggcgattt	300
ccgacaccgt	agaacagagc	aaggaggaga	tgaagagctt	ttaacagaaaa	gctccaaagc	360
aaccaatgtt	tgcactcgat	ttgaagactc	tccatcgat	gtaaaatggg	gtaaactgag	420
agattatcg	gtccccgagga	ttaaactggc	tcattttttt	gtatgagaat	ggcatcaatg	480
gtatccttgc	agatgaaatg	ggcttaggaa	agactttca	acaatttctc	t	531
<210>	122					
<211>	174					
<212>	DNA					
<213>	Homo sapien					
<400>	122					
tcgagcggcc	gcccggcag	gtctgccaac	agcagaggcg	gggcctccgg	catcttcaaa	60
gcacctctga	gcaggctcca	gcctctggc	tgcgggaggg	gtctggggtc	tcctctgagc	120
tcggcagcaa	agcagatgtt	atttctctcc	cgcgacctcg	gccgcgacca	cgct	174
<210>	123					
<211>	531					
<212>	DNA					
<213>	Homo sapien					
<220>						
<221>	misc_feature					
<222>	(1) ... (531)					
<223>	n = A,T,C or G					
<400>	123					
agcgtggtcg	cgcccgagg	cctcaaccaa	gagggttgat	ggcctccagt	caagaaactg	60
tggctcatgc	cagcagagct	ctctcctcg	ccagcaggcg	ccatgcaagg	gcaggctaaa	120
agacctccag	tgcataaca	tccatctagc	anagagaaaa	ggggcactga	agcagctatg	180
tctgccagg	gttagggct	cccttgcaga	cagcaatgct	acaataaaagg	acacagaaaat	240
gggggaggtg	ggggaaagccc	tattttata	acaaagtcaa	acagatctgt	gccgttattt	300
ccccccagaca	cacaagtata	aaaaaaacca	tgcttgggt	ttctgccaag	atggaatatt	360
cctccttcct	aanttccaca	catggccgtt	tgcaatgctc	gacagcattg	cactggctg	420
cttgtctctg	tggtctggc	accagtagct	tggggcccat	atacacttct	cagttcccac	480
anggctttag	gccnangggc	angctccat	tttcaagcac	cacgaaggaa	g	531

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<210> 124
<211> 416
<212> DNA
<213> Homo sapien

<400> 124
tcgagcggcc gccccggcag gtccatctat actttctaga gcagtaaatc tcataaaattc      60
acttaccaag cccaggaata atgactttta aagccttcaa tatcaactaa gacaaaattat      120
gccaattctg atttctcaca tatactttaga ttacacaaaag ataaagcttt agatgtgatc      180
attgttaat gtagactttat ctttaaaggtt tttaattttaa aactacagaa gggagtaaac      240
agcaagccaa atgatttaac caaatgattt aagagtaaaa ctcactcaga aagcattata      300
cgtaactaa tatacatgag catgattata tacatacatg aaactgcaat ttatggcat      360
tctaagtaac tcatttaagt acattttgg catttaaaca aagatcaa at caagct      416

<210> 125
<211> 199
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(199)
<223> n = A,T,C or G

<400> 125
agcgtggtcg cggccgaggt gctttttttt tttttttttt tttttttttt gctattctaa      60
aggggaaggc cccttttat taaacttgc cattttactt tccttttttc anaatgctaa      120
taaaaaactt ttgtttatac ttaaaaaaaaac cataaatcan acaaacaaaaa gaaacgattc      180
caacatcact tctgngatg      199

<210> 126
<211> 490
<212> DNA
<213> Homo sapien

<400> 126
cgtggtcg gcccgggtcc agtgctcta agtggattgg atatgggtgg agtggcacag      60
actggatctg ggaaaacatt gtcttatttg ctccctgcctt ttgtccacat caatcatcag      120
ccattcttag agagaggcga tggcctatt tggtgggc tggcaccaac tcgggaactg      180
gccccaaacagg tgcagcaagt agtgcgttattgttagag catgtcgctt gaagtctact      240
tgtatctacg gtgggtgtcc taagggacca caaatacgtt atttggagag aggtgtggaa      300
atctgtatttgc caacacccctgg aagactgtt gacttttagt agtgtggaaa aaccaatctg      360
agaagaacaa cctacccctgt ccttgatgaa gcagatagaa tgcttgatat gggcttggaa      420
ccccaaataa ggaagatgtt ggatcaaata agacctgata ggcaaaactct aatgtggagt      480
gcgacttggc      490

<210> 127
<211> 490
<212> DNA
<213> Homo sapien

<400> 127
cgtggtcg gcccgggtcc gcccgggtct ggagatctga gaacgggcag actgcctcct      60
caagtgggtc cctgaccctt gaccccccag cagcctaact gggaggcacc ccccagcagg      120

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ggcacactga cacctcacac ggcaaggat tccaacagac ctgaagctga gggtcctgtc	180
tgttagaagg aaaactaaaca agcagaaaagg acagccacat caaaaaccca tctgtacatc	240
accatcatca aagacaaaaa gtaataaaaa ccacaaagat gggaaaaaaa cagaacagaa	300
aaactggaaa ctctaaaaag cagagcacct ctccctttcc aaaggaacgc agttcctcac	360
cagcaatgga acaaagctgg atggagaatg actttgacga gctgagaaaa gaacgcttca	420
gacgatcaaa ttactctgag ctacgggagg acattcaaac caaaggcaaa gaagttgaaa	480
actttgaaaa	490
<210> 128	
<211> 469	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(469)	
<223> n = A,T,C or G	
<400> 128	
cgtggtcgcg gccgagggtgc tttttttttt tttttttttt tttttttttt tgctgattta	60
ttttttctnt ttatttttac atacaatgta taaacacata aaacanaaaaa cagtagggat	120
cctctaggat ctctaggan acagtaaaagt anaaagaggt ctcanaaaaca tttttttaaa	180
gtacaagaca ttcagnngtc ggcggaaagg cgtaaaaggt ttanagccag canatagctg	240
nactaaaggc tccgtctntn tccccanagc caggacaacc ccaggaggt ntccattagc	300
agccagtcca cgccaggcagg atgctgcgga aaaagctcta tgctganaac attcccccttg	360
atggaaagaa gggcaacaca aaagggttaa ctaanagctc cttectctcg tgagggcgac	420
aactgaggaa cagaaaagga gtgtcccatg tcacttttga ccccccctcc	469
<210> 129	
<211> 419	
<212> DNA	
<213> Homo sapien	
<400> 129	
gcgtggtcgc ggccgagggtc tgatttcat taaaatattt cagagctata gcatttgcc	60
ccatgctcaa atccacacca ttggggctta agccgctcat gccaacatta gcaaattgaca	120
tgcagttaa tccagagatc actgcttctg ggctgatgca tgccaaacaca ctggcgtgat	180
ccacgttagt tgcatttttc ttcaactttag tgggagaatc aatttttact ccaaggcttc	240
ttagttgctt aagagttgca ttaaggacac aatctttgtc caccagtctt gaatgatgtg	300
tttttttctt tgtatggtaa acgttttggg ttctggtgca ttcatgactg ataattactg	360
ctttggtaga cggctgctca agtttccttg gaggaactat ttaataggtg ggttacttg	419
<210> 130	
<211> 354	
<212> DNA	
<213> Homo sapien	
<400> 130	
agcgtggtcg cggccgagggt ccatctgagg agataaccac atcactaaca aagtgggagt	60
gaccccgccag agcacgctgt ggaattccat agttggtctc atccctggtc agtttccaca	120
tgtatgatgtt ctatctcga gaggcggaga ggatcatgtc cgggaactgc ggggttagtag	180
cgatctgggt tacccagccg ttgtggccct tgagggtgcc acgaagggtc atctgctcag	240
tcatggcggc ggcgagagcg tgtgtcgctg cagcgacgag gatggcactg gatggcttag	300
agaaaactagc accacaacctt ctccgtccgc acctgccccgg gcggcccgct cgaa	354

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<210> 131
<211> 474
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

<400> 131
cgagcggccg cccgggcagg tctggcagca gcttcctctg gaataattga cagctttgtg      60
ctggcctgact aaaatttcaa atgacaacccg ctgaatgtaa aatgatgtac ctacaatgag     120
agagatttag gaataactatc tgtaatcca tagatgtaga aacaaaaacaa actacagaat     180
gaaaacaaac ttattttaaa ccaaagaaac aaatgtatcc aaaatatagt ccatgatata     240
tttgattact agtataacca cagttaaaaa cttaaaaaaaa aaaattgaca tttttgtaa     300
tgggtactaa tggattata aaaggtttct gtttccaaag atgttattgg ggtccacata     360
ttcccttgaag acttcagcat cccaaagccc gacatcagag atacttcct ttagccattg     420
nttcccgtaa ctggccact ccatggtcat gtgacaggtt tcccttcatt agca      474

<210> 132
<211> 474
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(474)
<223> n = A,T,C or G

<400> 132
ggccgagggtg gggaaattcat gtggaggtca gagtggaagc aggtgtgaga gggtccagca      60
gaaggaaaca tggctccaa agtgttttag tccattggca agttttggct ggccttagct     120
gttgcaggag gcgtggtaa ctctgccta tataatgtgg atgctggca cagagctgtc     180
atcttgacc gattccgtgg agtgcaggac attgtggtag gggaaagggac tcattttctc     240
atccccgtggg tacagaaacc aattatcttt gactgccgtt ctcgaccacg taatgtgcca     300
gtcatcactg ttagcaaaga tttacagaat gtcaacatca cactggcat cctttccgg     360
cctgtcgcca gccagttcc tcgcacatcc accagcatcg ganaggacta tgatgaaccg     420
tgtgctgccc tccatcacaa ctgagatcct caagtcatgt gtggctcgct ttga      474

<210> 133
<211> 387
<212> DNA
<213> Homo sapien

<400> 133
tgctcgagcg gcccggcgtg tgatggatat ctgcagaatt cggcttagcg tggtcgccc      60
cgaggtctgc gggccctta gcctgcctg cttccaagcg acggccatcc cagtagggga     120
ctttcccaaca ctgtgcctt acgatcagcg tgacagagta gaagctggag tgccctcacca     180
cacggcccgaa acacagcggg aagtaactgg aaagagctt aggacagctt agatgccgag     240
tgggcgaatg ccagaccaat gataccaga gctacctgcc gccaacttgt tgagatgtgt     300
gtttgactgt gagagagtgt gtgtttgtgt gtgtgttttgc ccatgaactg tgccccccagt     360
gtatagtgtt tcagtggggg agaactg                                387

<210> 134

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<211> 401
 <212> DNA
 <213> Homo sapien

<400> 134
 gggcccccgg gcaggtctga tgaagaacac gggtgtgatc cttgccaatg acgccaatgc 60
 tgagcggttc aagagtgttg tggcaactt gcacggctg ggagtccaca acaccattat 120
 cagccactat gatgggcgcc agtccccaa ggtgggggg ggcttgacc gactactgct 180
 ggtatgtccc tgcagtggca ctgggtcat ctccaaggat ccagccgtga agactaaca 240
 ggtatgagaag gacatccgtc gcttgtgctc acctccagaa ggaagttgtc cctgagtgt 300
 attgactt gtcaatgcga ccttcaagac aggaggctac ctggtttact gcacctgttc 360
 tacacagtgc agacctctgc catggcagaa caggggaagc t 401

<210> 135
 <211> 451
 <212> DNA
 <213> Homo sapien

<400> 135
 ggtcgccggc gaggtctgtt cctgagaaca gcctgcattt gaatctacag agaggacaac 60
 taatgtgagt gaggaaagtga ctgtatgtgg actgtggaga aagttaagtca cgtrggccct 120
 tgaggacctg gactgggtta ggaacagttt tactttcaga ggtgagggtgt cgagaaggaa 180
 aagtgaatgt ggtctggagt gtgtccctgg ctttggctcc acagggtgtg ctttcctctg 240
 gggccgtcag ggagctcata ccttgcgttgc tgccaggggtg gggtaaccggg gtttgacact 300
 gaggagggtt acctgctggc tggagccggca gaacagtggc cttgatttgc cttttggaaag 360
 attttaaaaa caaaaaaagca taaacattct ggtccttcac aatgctttct ctgaagaaaat 420
 acttaacggc aggacttctc cattcaccat t 451

<210> 136
 <211> 411
 <212> DNA
 <213> Homo sapien

<400> 136
 gggcccccgg gcaggtctga atcacgtaga atttgaagat caagatgtg aagccagagt 60
 tcagtagatgag ggttttcgac ctggatgtt tgcgtccgtt gagattgaaa atgtccctg 120
 tgaatttgcg cagaactttt acccccttta cccattttt cttgggtggct tggcaacac 180
 tgagggaaat gttggacatg tgcagggtggg tccctttgcgt gcttattttgg tgcctgaggc 240
 tctgtggatt tccccctccat caatcatctt accctctcat cccctcaga tgcgtctgaa 300
 gaaacatctc tggataaga aaatcctcaa gtcccaagat ccaatcatat ttctgtagg 360
 gtggaggaat ttccagacca tcctgctcta ttatatccga agaccacaat g 411

<210> 137
 <211> 211
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(211)
 <223> n = A,T,C or G

<400> 137
 cggccgccccgg ggcaggtcgg ttgggtgcggc ctccattgtt cgtgttttaa ggcgccatga 60
 ggggtgacag aggccgtggc cgtgggtggc gtttgggttca cagaggaggc ccaggaggag 120

ggttcaggcc ctgtcacca catatccat ttgacttcta tttgtgtcaa atggccttc 180
cccggntcaa gccagcacct cgatgaaact t 211

<210> 138
<211> 471
<212> DNA
<213> Homo sapien

<400> 138
gccggccggg caggtctggg ctggcgactg gcattccaggg cgtaactgca aatctatgct 60
aggcggggtc tcccttctgt gtgttcaagt gttctcgact tggattctta actatttaa 120
aaaatgcact gagtttggtt taaaaaaccaa ccacccaaat ggatttcaac acagctctaa 180
agccaagggc gtggccggct ctcccaacac agcgactcct ggaggccagg tgcccatggg 240
cctacatccc ctctcagcac tgaacagtga gttgatffff ctttttacaa taaaaaaaagc 300.
tgagtaatat tgcataaggag taccaagaaa ctgcctcatt ggaacacaaa actatttaca 360
ttaaaaaaaa agcctggccg caggctgcgt ctgcccacatt tacagcacgg tgcgatgcac 420
acggtgacca aaccacggag gcaagttct ggcactcaca ccacgaccccg c 471

<210> 139
<211> 481
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(481)
<223> n = A,T,C or G

<400> 139
gtcgccggcc aggtctgttc tttagctcag atttaaacct gctgtctctt ctttatttgc 60
agaatgaatt cccagtccct gagcagttca agaccctatg gaacggcag aagttggtca 120
ccacagtgac agaaatgtct ggataagcga agtgcacgt ggttcttgc cttcccttca 180
caccatggga taaatctgta tcaagacggt tctttcttag atttctctta cttttttgtct 240
cttaaaaactg cttctctgtct ctgagaagca cagctacccgt ctttctactga aatataccctc 300
aggctgaaat ttgggggtgg atagcagggtc agttgatctt ctgcaggaag gtgcagctt 360
tccatatcag ctcaaccacg ccgnacgtcc attcttaagg aactgccac taggactgat 420
gatgcatttt agcttttgag cttttggggg gtattctacc aaccaacagt ccatttgaa 480
a 481

<210> 140
<211> 421
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(421)
<223> n = A,T,C or G

<400> 140
gtcgccggcc aggtttccca tttaagaaaa atagatcttg agattctgat tctttccaa 60
acagtccccct gctttcatgt acagcttttt ctttacctta cccaaatcc tggccttgaa 120
gcagtttcc tctatggctt tgcccttctg attttcttag aggctcgagt cttaatata 180
acccaaatg aaagaaccaa ggggaggggt gggatggcac tttttttgt tggtcttggtt 240
ttgtttgtt ttttgttgg ttgggttccg ttattttta agattagcca ttctctgctg 300

41

staaaaacccat acataatgtc aatttttaac cataatttg acatgattga gatgtacttg	360
aggctttttt gnttaattt agaaaagact ttgcaattt ttttttagga tgagcctctc	420
c	421
<210> 141	
<211> 242	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(242)	
<223> n = A,T,C or G	
<400> 141	
cgantngccc gccgggcan gtctgtctaa nttntcang gaccacgaac agaaactcgt	60
gtttcacccga anaacaatat cttaaacatc gaanaattt aatattatga aaaaaaacat	120
tgcggggat aaaaataa nnaaaaggaa aggaaaactt gaaccttatg taccgagcaa	180
atccaggtct agcaaacagt gctagtccta nattacttga tntacaacaa cacatgaata	240
ca	242
<210> 142	
<211> 551	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(551)	
<223> n = A,T,C or G	
<400> 142	
agcgtggtcg cggcnccgang tccacagggc anatattctt ttagtgtctg gaattaaaaat	60
gtttgagggtt tangtttgcc attgtcttc caaaaaggcca aataattcan atgtaaaccac	120
accaagtgc aacctgtgt ttcttattca cgtactgttg tccatacagt tctaaataca	180
tgtgcagggg attgttagcta atgcattaca cagtcgttca gtcttctctg cagacacact	240
aagtgtatcat accaacgtgt tatacactca actagaanat aataagctt aatctgagggg	300
caagtacagt cctgacaaaa gggcaagttt gcataataga tcttcgatca attctctctc	360
caagggggccc gcaacttaggc tattattcat aaaacacaaac tgaanagggg attggttttt	420
ctggtaaatc atgtgntgct aaatcatttt ctgaacagt gggtctaaat cantcattga	480
tttagtggca gccacctgccc cggcggccgn tcgaagccca attctgcaga tatccatcac	540
actggcggcc g	551
<210> 143	
<211> 515	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(515)	
<223> n = A,T,C or G	
<400> 143	
cgagngggccc gccccggcag gtatttcac aaactcaaca aaggcactac atgagacttc	60

acattccccct agtccaaatag ctgacaaaatt tttgcaacgt tctgcaatgc gaattaactc	120
ttcataagt ggccgtataatc catttgcaca cactactagt tcaaccagtc tagggcatgt	180
cattcccaca cggccaaagca catctttgtct tactgatctc ccaaagtaca gatgggtggc	240
aggtatttca tagcgaaaaga aggggtcaaaa ttcttcttca tataaaaaaa aataacatcac	300
taagttcact ttgggtgaat gtctgatgaa agcatccag ctactcttct gaatagtgatg	360
gaaggtgtgtc tgtccaggat tctcaactgac tacatcaatg cgcaaatgtt ctaatcgAAC	420
atgttttca gaagacaatg caagtaacaa ctcatcactc aataagtgg aagttcaggg	480
ctagttctct taagccngna cactgatcag cacac	515
<210> 144	
<211> 247	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(247)	
<223> n = A,T,C or G	
<400> 144	
tgcatctct ntggatgcan acctgcccgt tggtagggac tntgctcaca cggAACATGG	60
acggttacac ctgtccgtg ggtgacgtcc accagcttct ggatcatctc ggcgnnggtg	120
ttgtggaagg gcagactatc cacctccatg cnCACGATGC ccGANACGCC actccggact	180
ntgtgctgca ccaanatgcc cagcatnta tcttcaagca nagcaattat cagggtcctt	240
ggcacac	247
<210> 145	
<211> 309	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(309)	
<223> n = A,T,C or G	
<400> 145	
cgtgggtcgc ggcccgangt ctgctgtAAC aaaacaccat agtctggca gctcatAGAC	60
aatggaaattt tatttctcac gcttctggag gctggattcc aagatcaagg ttccaggaga	120
ctcagtgtct ggcaagggtct cgggttctgc ctcanagatg gtccatctg gctgtgtcct	180
cacaagttagg aaggtgcaag aagctccccct caggctctgt ctgtaagaca ctgatccat	240
tcatganggg gaaacgtaat gacctaattca gcccccagag accccacttc taacaccatc	300
accttgggg	309
<210> 146	
<211> 486	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(486)	
<223> n = A,T,C or G	
<400> 146	

agcgtgggtc	gcggcncgac	gtcctgtcca	tat	ttcacag	ccc	gagaact	aatacaagat	60
gctgacatca	tat	tttgtcc	ctacaactat	cttctanatg	caca	aaataag	ggaaagtatg	120
gattaaatc	tgaaagaaca	ggttgcatt	ttanatgaag	ctcataacat	cgaggactgt			180
gctcggaaat	cagcaagtt	cagtgtaca	gaagttcagc	ttcgggttgc	tcgggatgaa			240
ctanatagta	tggtcaacaa	taatataagg	aaganagatc	atgaacccct	acgagctgtg			300
tgctgttagcc	tcattaattg	gn	tagaagca	aacgctgaat	atcttgnana	ang	agantat	360
gaatcagctt	gtaaaatatg	gagtggaaat	gaaatgctct	taacttaca	caa	aaatgggt		420
atcaccactg	ctactttcc	catttgcng	gtaagatatn	ttttctacct	gngaaacgta			480
tttaag								486
<210> 147								
<211> 430								
<212> DNA								
<213> Homo sapien								
<220>								
<221> misc_feature								
<222> (1) ... (430)								
<223> n = A,T,C or G								
<400> 147								
gccggccggg	cangttcgac	attacntnga	gttccatgat	gtacaattct	ttcacgaaaa			60
acaatgaatg	caagaatttg	aggatctcct	tactcctccc	ttttacagat	ggtctctcaa			120
tcccttcttc	ttccttctca	tcttcatctt	cttctgaacg	cgctgccggg	taccacggct			180
ttctttgtct	ttatcgtag	atgaagggtga	tgcttctgtt	tcttctacca	taactgaaga			240
aatttcgctg	caagtctctt	gactggctgt	ttctccgact	tcgccttnt	gtcaaacgng			300
agtctttta	cctcatgccc	ctcagttca	cagcatctc	atctggatgt	tnatttctca			360
aagggctcac	tgagggaaact	tctgattcan	atgtcgaana	gcactgttyaa	gttttctctt			420
cattttgctg								430
<210> 148								
<211> 483								
<212> DNA								
<213> Homo sapien								
<220>								
<221> misc_feature								
<222> (1) ... (483)								
<223> n = A,T,C or G								
<400> 148								
ccccggcagg	tctgtgttgn	tttcaaccg	gtgtcctccc	cagcgtccag	aanangggaaa			60
tgtggagegg	gtgatgatga	cccctcgctg	tcctgtcacc	tcctgcacag	cttcgttatgt			120
gggtctggtc	tgggaccacc	cgtacagggt	gtgcacgttg	tagtgcctca	cggggggagct			180
gtccggcagg	atctgtgac	tctccatgca	cagagtcttg	ctgctcaggc	ccttgcctt			240
agatccaaa	tatggcatat	agggtgggggt	tat	tttagcat	ttcattgtctg	cag	ccccctga	300
cagatccatc	cacaaaattt	gatggctcat	tcatatcaat	ccacaatcca	tcaaacttca			360
agctcttctc	tggntctcga	nggtttgcat	agaactcttc	tatcttttc	ttccaccacg			420
canacccctcg	ncgcgaccac	gctaagccga	attctgcana	tatccatcac	actggcggcc			480
gct								483
<210> 149								
<211> 439								
<212> DNA								
<213> Homo sapien								

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<220>
<221> misc_feature
<222> (1)...(439)
<223> n = A,T,C or G

<400> 149
ctttcacgaa nacaatgaat gcaagaattt gaggatctcc ttactcctcc ctttacaga      60
tggctctca atccctctt ctccctctc atcttcatct tcttctgaac gcgctgccgg      120
gtaccacggc tttctttgc tttatcgtga gatgaagtg atgcttctgt ttcttctacc      180
ataactgaag aaattcgct gcaagtctct tgactggctg tttctccgac ttgcctttt      240
tgcaaacgtg agtctttta cctcatgcc ctcagcttcc acagcatctt catctggatg      300
ttcatttctc aaagggtca ctgagggaaac ttctgactca catgtcgaag aagcaactgng      360
agtttctctt catttgcgtc aaanttgctc ttgtctggct gngctctcag accacccatt      420
tggctgcata ggggctgac      439

<210> 150
<211> 578
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(578)
<223> n = A,T,C or G

<400> 150
ggcncgcccc ggcangtcca ctccactttt gagctcttag ggaatacctt caggagggac      60
agggtcaggc agtcctggca gctccgcagc agagattcac attcatttag agacttgttg      120
tccagtgcaa tgccattgtat cgcaacgatc ctgtctccca cagcaaggga cccttcttta      180
gcggcagggg ttcaggcag cacagcggca gcatacactc catttccag actgatgcca      240
ctgtcttttct gtccactgan gttatgtgc ageggcgtga ccacccccc acccagggac      300
ttcctccgccc gcacgaccat gttatgtggc cccctnccca ttgaggagcg ccttgatggc      360
ctgcttcttg nccttggta tgaagtccac atcgggtgatt ctcacagcca gtcattgacc      420
cttaagcggn catcagcaat gcttctttg gccacttttag ngacaaaatat gccacagtcc      480
ccgggaaaca agggtcattc acaccttctg gcatatcaaa cacctcgcc gggancacta      540
agccgaattt tgcagatatac catcacactg gngggccg      578

<210> 151
<211> 503
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(503)
<223> n = A,T,C or G

<400> 151
cgagcggccc gcccggcag gtctggaga tcagcgactg ctgccacgtg cccagaaatg      60
gctcgccctt tcactacagc ggaatgcaat gagggtgggt gagaagatga tgggtcggtt      120
atttcattcc ttttctttt acaacttcac ttccagagac ttccagcttc catgtctgtct      180
gtgctgtgga acccagagtg ctctgcctg gatggctgag aatccctgg accctggaaag      240
cacctactcc atgatggccc ggtatagtgc aggctcaata taatcttccc ggtatcttga      300
gttataact cgttgcgtt tttttcttgc cttaacctct ttctctgtga aaatcttatt      360

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gaagcgcatg tctgaagcta ctgacagtct anatttact ctcttggaa gctcttcata	420
cagtgttat acatcatctc tcttaaccac aagttggagc catncttaaa cttcacctgg	480
tacatttgga tagggtggga ggc	503
<210> 152	
<211> 553	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(553)	
<223> n = A,T,C or G	
<400> 152	
agcgtggtcg cggcccgagg tccactgagc tccgccttcc ccgggctccc tgaggaagca	60
gagtccctgac ttccaggaag gacaggacac agaggcaaga actcagcctg tgaggctctg	120
ggtgtggctctt gaggccagag gacgccttcc gcgcattcatg gtcagcata gtccttctgg	180
cttccccagcc ccgggcccggaa cgttcggtt aataagcaga gcagttattc ggcteetggc	240
aggagctccc ccgttagttt ccacgttgcg agcacattca tacttaagac tgnttcttt	300
tgtgttttaa gcgctgtct ctgttagaaa ctgaaatgtt aacagaaatg cagacatgcc	360
ccggccggccg ctcgaaagcc gaattctgca gatattccatc acactggccgg ccgcctcgagc	420
atgcatcttag angggccaaat tcgcccataa gtgagtcgna ttacaattca ctggggcccg	480
ntttacaacg tcgtgactgg gaaaaaccctg cggtaccac ttaatcgct tgcagnacat	540
cccccttcg cca	553
<210> 153	
<211> 454	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(454)	
<223> n = A,T,C or G	
<400> 153	
tcgagcggct cggccggca ggtccaccta gcatggctcc tctaaacacg caactcagcg	60
agggggacccc cttcacctct ggcaagagag ctgggttagat cagaaacttg gtgacacctg	120
gctagcacag agcaggctca cttgtcttgg tcccactacc cagattcctg cagacattgc	180
aaaccaaataa aaggttgtt aatgaccctt gtcccccagcc acttggggat gatatcatctg	240
ctctgcagtg gaatgcctgt gtgtttgagt tcactctgca tctgtatatt tgagtataga	300
aaccgantca agtgtatctgt gcatncagac acactggggc acctgancac agaacaaatc	360
accttaacga tctgaaatga aactgnganc antgcccggc tgggtgggtc tgganaaaact	420
cccggncttct tggggaccc acc	454
<210> 154	
<211> 596	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(596)	
<223> n = A,T,C or G	

<400> 154
 agcgtggtcg cggcccgang gcccctcct gantganggg aaggacgtg gggcgccca 60
 cggcaggatt aacccatt tcagctaatac atggagaga ttaaagtctc tcctgattat 120
 aactggtttta naggtacagt tccccctaaa aagattattg tggatgtga tgacagtaag 180
 atatggtcgc tctatgacgc gggcccccga agtatcaggt gtcctctcat attcctgccc 240
 cctgtcagtg gaactgcaga tgtcttttc cggcagattt tggctctgac tggatgggg 300
 taccgggtta tcgcttgca gtatccagtt tattgggacc atctcgagtt cttgtgtatgg 360
 attcacaaaaa ctttanacc atttacaattt ggataaaattt catcttttgcgcctttt 420
 gggangctt ttggccana aatttgctga atacactcac aaatctcta gaagccattc 480
 cctaattcctc tgcaattcct tcagngacac ctctatcttc aaccaacttg gactggaaac 540
 agctttggct gatgcctgca tttatgctca aaaaatagtt cttggaaattt ttcatac 596

<210> 155
 <211> 343
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(343)
 <223> n = A,T,C or G

<400> 155
 ctgcgantgg cnccggggc cangtctgcc tggtttttga ccngcggc tatttagnct 60
 ctggctctgt ttccggagct caaggnaaaa atcttgaana actcgagcag cttctgtgg 120
 tagccttggg tacacataact gcccggcata gccaatgtac tttctcaata gctgggg 180
 aatgggatct attgttctc caggaaccac cttagtctt tctgataatg gcttctcaga 240
 aactacttca agtacgaaag tatttgaatc ttgactatnc atacgagcta ctgtggcact 300
 gctaattgggn tctctgtnt ccagcttta ttgcaatcac atg 343

<210> 156
 <211> 556
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(556)
 <223> n = A,T,C or G

<400> 156
 tcgagcggcc cgccccggca ggtctggcac cacncagatc gattaactgg ctcatctgat 60
 ctcgtggccc ccaccccttga actgacttag cacaaaagga cacctcaatt cctttagatt 120
 tcatctccga cccaaaccat caacaccctt gactcaactgg cttcccccctt cccaccaaatt 180
 tatcctttaaa aactctgatc cccgaatgtc cagggagatc gatggatgtca ctaataagac 240
 tccagtcctcc tgcacaagca gctctgtgtat cttttcttatttcaatttcttgc 300
 aaatcggctc tggtagggcg gcggagaag tgaacctgtt gggcggttac cacctctgtc 360
 gtgtgtgaca gttgnnttga atctctaattt gctcagtaca gatccacatg cagggttaagt 420
 aagaagctt tgaagaaaat ggaaagtctt aagtgtatggc ttccaaagaaa tcaaaccctac 480
 attaatttgg gaacaacggc cttacgtat cacaaatgaa gagactgacn aagtaaatca 540
 acttggctt ttctta 556

<210> 157
 <211> 333

<212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)....(333)
 <223> n = A,T,C or G

<400> 157
 ggtccacaaa aatatataa ataagctgga tatataaaan caaacactta acatngncan 60
 cattccttca gttattcaaa ctcactgata nctaacnccc agnagttggg attcttggaaag 120
 acttcctaag ctaaaagtat atttacatat ttacaacaca ngtaaatata acngaagaac 180
 tacttcaaat aangnnngaaa ttccagaatt ctanagattt atagctatacg ntnacaanta 240
 tcaccaattt gtttgcattc aanngnccag cactacttat gannaangtt taactannaa 300
 accaaaaggg gagaaaacctt ggnagggaaa nat 333

<210> 158
 <211> 629
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)....(629)
 <223> n = A,T,C or G

<400> 158
 tcgagcggcc gcccgggcag gtctggtaca tttgtgcgag gtccggcact ctgttctcat 60
 ccagtaagtg gtgcggccct ttctgcagaa ttgctgttaa atgttcttct aatagctgtt 120
 tctccacaca agcaatcgtt gggttctgtg tgctgtggtc caagtaagtg attactctgt 180
 ctcccttcttcc ttcttaagcgtt ttacttacat ggttaagata ttcttggacc tctttccct 240
 gcatttaacctt ttggccttcg gcagcatata agcaatttgc ctcttccaaa aatttcagtt 300
 caaatgaatcttatacacc tgcaaggcgtt acagcatgcc caggnaggct ccgcaacagg 360
 ctccgggtcca cggcctcgcc gctccctctcg cgctcgatca gcagtaggat tccatcaatg 420
 gttttactttaatcactaata atatgggttc taaacagttc taatcccata 480
 tcccagatgg agggcagcgtt ggagttctgc agcacatagg tgccgtccaa gaacagggaa 540
 atgcttctga tcatgaatca ttgnctggc aatggtccttgc ccagcacgtt gtaatcttcc 600
 ttttaaaaat aaacccttat cttaaacgtt 629

<210> 159
 <211> 629
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)....(629)
 <223> n = A,T,C or G

<400> 159
 tcgagcggcc gcccgggcag gttcttagagg ganaatctgg ctgatttggg aataaaaat 60
 aatcgaatataat tcaacaccat gaagataaaat cttatttgg aaatctactg accttaataac 120
 cccaagcttg ccctgaataac ttgttggg attggaaat atcaaaaaag gtttagtattt 180
 ttgtttagt taggatacta aaaggatatt agttacccaa gagatccaaat ttgtttttct 240
 gatgaatagt gttcgttataa atgaagcgtt cttaagatgt actaataatt tcaaagtgt 300

tttcgtcta ttcttaatat ttttaatta ttatattta agagtttat accttgagca	360
gatacatga tccgccttag tgagaggaca atttctgatt gatttttc tttcaggcc	420
atctcaccc ttcattctt tttacattt gaagcaggta atataatggg ttataacttt	480
aaaagataga catggtcca tgaagttgg ggaagttggg tgaattatcc cattctagtt	540
acagangagc ttcccttaaa tgccctttac ttctangttt ggtcaagaag tcattttctg	600
agtaaaaagtt atttcatat atgttgggg	629
<210> 160	
<211> 519	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(519)	
<223> n = A,T,C or G	
<400> 160	
tcgagcggcg cgccccggca ggctctgctgg gattaatgcc aagtnttca gccataagg	60
agcggaaatct agcagaatcc agattacatc caattccat cacgcggtgt ttgggtatc	120
cacttagttt ccagataaca tacgtaagaa tgtccactgg gttggaaacc acaattatga	180
tgcataatcagg actgtacttg acgatcttag gaataatgaa tttgaagaca ttaacatttc	240
tctgcaccag attgagccga ctctcccctt ctgtctgacg gactcctgca gttaccacta	300
caatcttana attggggggg tcacagaata atctttatct gccacaattt taggtgctga	360
agaaataaagc tcccattgtc cagatccatc atttctnctt taagtttac ttccaaaaca	420
tccacaagan caangttcat cagccagaga ctttcccaga atgctgatag nacacgccc	480
accaacttgtt ccaacancca ctacagcgat cttattgg	519
<210> 161	
<211> 446	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	
<222> (1)...(446)	
<223> n = A,T,C or G	
<400> 161	
cgagngggcc gccccggcag gtccagtaag ctttnacga tgatggaaa ggttatgca	60
ggcccagcg gtacaacgag ctgtttctac atcatttta ttctgcatgg tacgtacaat	120
agcagacacc atctgaggag aacgcattgt agcgtgtctg gaagcttctt ttttagaaag	180
ctgatggacc ataactgcag ctttattaaac caccacctgg ttctgcat ttagcagttt	240
tgtcagttca gggattgcac gtgtggcang ttctgcatca ttgtatagt taatcaagtt	300
tacaactggc atgtttcagc atctgcgtatggctcagcaa acgctggaca ttantggat	360
gagcagcatc aaactgtgtt natggatct gcatgccctc atctaattgtc tcaggaaaca	420
tagcagctcg taccctctga gtcgat	446
<210> 162	
<211> 354	
<212> DNA	
<213> Homo sapien	
<220>	
<221> misc_feature	

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<222> (1)...(354)
<223> n = A,T,C or G

<400> 162
agcgtngtcg cggcccgang tcctgggaag ccttnttgc tgaggctcac agcctctgtc      60
aggcggctgc gatatccagcg gtccaccagg ctctcatggc ctccgggctg ggaggngggt     120
gagggcacaa aaccctccc aaggccacga angcaact tggtgccatt ccanagctt     180
ttgcanaagt ggcgnaacc cagtatccgg ttcacatcca ggntgatgtc acgaccctgg     240
gacatgtang cacataatcc aaaccggaga gcatcggtgc cacattcacg aatccccgt     300
ggaagtcag ctttctgccc ttcttggcc ttctccacct cgctggatc cagg     354

<210> 163
<211> 258
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(258)
<223> n = A,T,C or G

<400> 163
ttttcncca agtccctttg ccngggatc tngactgaa tttaagacac ttctaatttag      60
ttataccca gcccgtcaaa attgctgggt ttatataata tattttgtct gcacgaagat     120
tttattattct gttggatgtat tctatttaa ttntattttat tctggccaaa aaagaacctt     180
ctccgctcgt caagagangc caatntgtct tgaaggacaa gagaaagatg ctaacacaca     240
cttcttctt cttgagga     258

<210> 164
<211> 282
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(282)
<223> n = A,T,C or G

<400> 164
ggaacatatt acttttaaat tacttgggtc aatgaaacat ttaataaaaa catttgcttc      60
tctatataat acgtatgtat aaaataagcc ttttcanaaa ctctggttct cataatcctc     120
tataaaatcan atgatctgac ttctaagagg aacaaattac agnaagggtt atacattnat     180
gaataactggt agtactagag ganngacgt aaaccactt actaccactt gcggaactct     240
cacagggtaa atgacaaaagc caatgactga ctctaaaaac aa     282

<210> 165
<211> 462
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(462)
<223> n = A,T,C or G

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<400> 165
 gcccgggcan gtcctgtaat cccagctact cangangctg agtcatgana atccgcctgaa 60
 tccggggaggt agaggccgca gcgagcaaag attaagccac tgcactccag tctgggtgac 120
 agagttagaa tctgtctgtt gtcctctgg cattggctcg aaatgggttt gtagaacatg 180
 ccacagaagg accagcana gcaacaaaatg gatttgtga angcttagct ccaaattggag 240
 cangcacact tgatgaagca cgctgtgtct gtgcagangc aaccactggc actgttccaa 300
 aaacattgtct gctagcatta ctttgaaag tatacgcatt actggaggtg gctgcanaac 360
 tgaaaacgct gtcttagttct gccanagctg catacttgnc tgaanatgca ctgactgac 420
 tggaaactga accacanaac caacaggacc tttacctgtg ga 462

<210> 166
 <211> 365
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(365)
 <223> n = A,T,C or G

<400> 166
 cgtgggtcgc ggcncgangt ctgaaaccaa tccagaacta aacatcagca cacaaaaat 60
 accaggatag atggaatcaa aagactctga agccaaaagg aggctaggaa gagcaactga 120
 acttagcaag ctgaggactt cagtgtccat catccgatcc tgcctgtaa caacaggct 180
 atatgataga gatattccat ctgagctgga ggccattatc cttagcaaac taacacagaa 240
 cagaaaaacca aatacatgtt ctcattttaga agtaggagct aaatgatgag aactcaagga 300
 cacaagaaaa ggaacaacag acactgggc ctacttgagg gtggagggtg ggaggaggga 360
 gaaga 365

<210> 167
 <211> 364
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(364)
 <223> n = A,T,C or G

<400> 167
 agcgtggtcg cggcgcgang tccagcccta gcttgcctgt gactccgcct tcactgggtg 60
 ctctctctaa aagtgtctga ctctttactg tatctcccaa ttcccactcc attgggttcca 120
 taagggggagg ggtgtctcac tcaacatgtt gttccctggta ccaagaactg gctgacgaaag 180
 ctgggtgccc tggctcatgc ctgtaatccc agcacttttggagggcaag aagggcggat 240
 cacctgaggt ctggaggttca agatcagcct gaccaacatg atgaaaccaa gtctccacta 300
 aaaatataaa acaatttagcc aggcattgtg gtgggtgcct gnaatcccag ctactggggaa 360
 ngct 364

<210> 168
 <211> 447
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1) ... (447)
 <223> n = A,T,C or G

 <400> 168
 cccgggcagg tcaaaaacca aaacctttca ttttagccca aaccagctca tgatttaggtta 60
 tacaaggata acagaaccag ttgtcaggac gagcatttga caagtaaaag caattcttgc 120
 aaagctgcag ttcatccagc tcatggcatg tgtctttata tagcatcctc gcaatgtcag 180
 ctgtctact gtctgctcca tagaaaatca cggtattgtg gagaagcaat tgggcatcag 240
 ctttgaactc ttcataaactt cggtatttcc cttcattcac tttctttaa atgggtggaa 300
 cgtccacaga cctcgcccgc gaccacgcta agcccgaatt ctgcagatat ccatcacact 360
 ggccggccgtt cgagcatggc atctagaagg cccaaattcgc ctatagngag tcgnattacc 420
 aattcaactgg ccgtcgnttt acaacgc 447

 <210> 169
 <211> 524
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (524)
 <223> n = A,T,C or G

 <400> 169
 cganngcgc gccccggcag gtcgtggcag cctttctggn tgctggacta ttgggattgg 60
 gtcatccaa cagagactgt atggatgtta gaatggaaaga cacatcatag gttggactcc 120
 aacggttctg aagtatgtcc agacatatac taccatctgc atagactaag aacaaagaag 180
 taggtacatt aaacgttaaca agaccactaa ggttttaaca ttatagacaa aacanaaaata 240
 gtcaganta ctttgctttt gaagttaaa gattcctatg ttgcttccc gtaactgcc 300
 taaaaagata agncataaacc accactagtg aaataatcan gatgatcaga gaatgtcana 360
 tggatcagt ataaaactgg angatattna gtgtcatcct ttggaaaagg ctgcctatn 420
 atccaggaaa tcanaaacat tnttgaacag ggnccctagc tatccacaga catgtggaa 480
 attcattttcc caaatngtag gctggatccc ctatctgaaa taac 524

 <210> 170
 <211> 332
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1) ... (332)
 <223> n = A,T,C or G

 <400> 170
 tcgancggcn cgcccgggca ggtgacaaac ctgttattga agatgttgt tctgtatgagg 60
 aanaanatca gaagggatgg tgacaagaan aanaanaaga agattaagga aaagtacatc 120
 gatcaagaag agctcaacaa aacaaagccc atctggacca gaaatcccga cgtatattact 180
 aatgangagt acggagaatt ctataanagc ttgaccaatg actggaaaga tcacttggca 240
 gtgaagcatt tticagttga nggacagttg gaattcagag cccttctatn tgtcccacga 300
 cgtgctccctt ttgatctgtt tganancaga aa 332

 <210> 171
 <211> 334
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(334)

<223> n = A,T,C or G

<400> 171

cgagnggcnc	gcccggcag	gtctgttgc	agcgacttaa	cagaaaagtc	tagacaaaca	60
taagcataaa	aaattacagt	cttctaccc	ttgggaatgg	ggagaaaaag	gaatctctac	120
cccaagacca	gaaataataa	gtctgttgc	tggcctgaa	catccagaat	tatggaggct	180
ttggcctgac	accacattan	aatttggct	ggaaatcaaa	ctttaganac	angagatcgt	240
aagccatttt	atactatcga	cctaaattcc	agtctaaccgg	ttcccttaca	aagttgcgga	300
aagccctctt	atatgctagc	tgttaggaaat	atag			334

<210> 172

<211> 439

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(439)

<223> n = A,T,C or G

<400> 172

agcgtggtcg	cggcccgang	tctgcctata	aaactagact	tctgacgctg	ggctccagct	60
tcatttcac	aggtcatcat	cctcatccgg	gagagcagtt	gtctgagcaa	cctctaagtc	120
gtgctcatac	tgtgctgcc	aagctgggtc	catgacaact	tctgggtgggg	cgagagcagg	180
catggcaaca	aattccaagt	tagggtctcc	aatgagcttc	ctagcaagcc	agaggaaggg	240
cttttcaaaag	tttgttagttac	tttggcaga	aatgtcgtag	tactgaagat	tcttctttcg	300
gtggaaagaca	atggatttcg	ctttcacttt	ctgccttaat	atccactttg	gtgccacaca	360
acacaatggg	atgnnttca	cacacttngn	accanatctc	tatgccagnt	aggccatttt	420
ggaagnactt	cganggtac					439

<210> 173

<211> 599

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(599)

<223> n = A,T,C or G

<400> 173

cgatngccg	cccgccagg	tcctgtaaaa	naggaaattc	agacatcgta	cgactcgtaa	60
ttgaatgtgg	agctgactgc	aatatttgt	caaagcacca	gaatagtgcc	ctgcactttg	120
cgaagcagtc	taacaatgtg	cttgtgtacg	acttgctgaa	gaaccattta	gagacacttt	180
caagagtagc	agaagagaca	ataaaggatt	actttgaagc	tcgccttgct	ctgcttagaac	240
cagttttcc	aatcgcatgt	catcgactct	gtgagggtcc	agattttca	acagatttca	300
attaccaacc	cccacagaac	ataccagaag	gctctggcat	cctgctgttt	atctccatrg	360
caaactttt	gggtaaagaa	gttattgtc	ggctctgtgg	accgtgtagt	gtacaagctg	420
tagttctgaa	tgataaaattt	cagttccctg	ttttctgg	tctcgctctg	ttgtccaggc	480
tggagtgcag	tgccgcggat	tacagctcac	tggagtcttg	acttcccagg	cacaagcaat	540

cctccccacct cagcctcccta actaacctggg actaaaaatg caccgccacc acattccgg 599

<210> 174
<211> 458
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(458)
<223> n = A,T,C or G

<400> 174

tcgatttggc cgccccggca ggtccatgcn gnttn gccccc attccccatgg ngccccacaa 60
ncccatcccc gaggcccaca tccccatgtt catgttcatg cccaccatgc cctggctcat 120
ccctgcgcgtg ttccccagag gggccatccc catggtgccc gtcattacac cgggcgtt 180
cataggcatg ggtcccccca ggagagggtt agnttgagge cggacaggaa gcatgttga 240
tggagaactg aggttccacag nctccaaaac tttgagtcat cacattcata ggctgctgca 300
tattctgtct gctgaatcca ttgtatncag tgatggctg ctggggnttt ggaaggctng 360
cataccaggt agtaagnntcg tctaggctga tgtttacacc tgggggtcaga ccaagtang 420
ggcaaggtt ttgctgactg attttctgga cccatata 458

<210> 175
<211> 1206
<212> DNA
<213> Homo sapien

<400> 175

ggcacgagga agttttgtgt actaaaaaag aaactgtcag aagaaaaaaga aataaaatca 60
cagtttagaga accaaaaaagt taaatggaa caagagctct gcagtgttag gtttctcaca 120
ctcatgaaaa taaaaattat ctcttacatg aaaattgtcat gttgaaaaaag gaaattgcca 180
tgctaaaaact gggaaatagcc acactgaaac accaatacca gggaaaggaa aataaaatact 240
ttgaggacat taagattttaa aagaaaaaga atgctgaact tcagatgacc ctaaaactga 300
aagaggaatc attaactaaa agggcatctc aatatagtgg gcagcttaaa gttctgtatag 360
ctgagaacac aatgtcaact tctaaattga agggaaaaca agacaaagaa atactagagg 420
cagaaaaattga atcacaccat cctagactgg cttctgtgt acaagaccat gatcaaattg 480
tgacatcaag aaaaagtcaa gaacctgctt tccacattgc aggagatgct tgtttgc当地 540
ggaaaaatgaa tggatgtg agtagtacga tatataacaa tgaggtctc catcaaccac 600
tttctgaagc tcaaaggaaa tccaaaagcc taaaaattaa tctcaattat gccggagatg 660
ctctaagaga aaatacattt gtttccaaac atgcacaaag agaccaacgt gaaacacagt 720
gtcaaatgaa ggaagctgaa cacatgtatc aaaacgaaaca agataatgtg aacaaacaca 780
ctgaacagca ggagtctcta gatcagaaat tatttcaact acaaagcaaa aatatgtggc 840
ttcaacagca attagttcat gcacataaga aagctgacaa caaaagcaag ataacaattg 900
atattcattt tctttagagg aaaatgcac acatctctt aaaagagaaa aatgaggaga 960
tatttaatta caataaccat taaaaaacc gtatatatca atatgaaaaa gagaaagcag 1020
aaacagaagt tatataatag tataacactg ccaaggagcg gattatctca tcttcattct 1080
gtaattccag tggatgtcact gttttgtt aataaaatgaa taaagaatga gaaaaccaga 1140
agctctgata cataatcata atgataatattt tttcaatgca caactacggg tggatgtct 1200
cgtgcc 1206

<210> 176
<211> 317
<212> PRT
<213> Homo sapien

<400> 176
 Met Gly Thr Arg Ala Leu Gln Cys Glu Val Ser His Thr His Glu Asn
 1 5 10 15
 Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala
 20 25 30
 Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys
 35 40 45
 Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala
 50 55 60
 Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg
 65 70 75 80
 Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr
 85 90 95
 Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu
 100 105 110
 Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp
 115 120 125
 His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His
 130 135 140
 Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser
 145 150 155 160
 Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu Ser Glu Ala
 165 170 175
 Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr Ala Gly Asp
 180 185 190
 Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln Arg Asp Gln
 195 200 205
 Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met Tyr Gln Asn
 210 215 220
 Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Gln Glu Ser Leu Asp
 225 230 235 240
 Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu Gln Gln
 245 250 255
 Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys Ile Thr Ile
 260 265 270
 Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu Leu Lys Glu
 275 280 285
 Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys Asn Arg Ile
 290 295 300
 Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Val Ile
 305 310 315

<210> 177

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in the Lab

<400> 177

ccaaatcatct ccacaggagc

20

<210> 178

<211> 1665

<212> DNA
 <213> Homo sapien

<400> 178

gcaaactttc aagcagagcc tcccagaag ccatacgcttc tcgaggctgc cattgaaatg	60
caaaaagtctt ttccaaataa agccttgaa ttgaagaatg aacaaacatt gagagcagat	120
cagatgttcc cttcagaatc aaaacaaaag aagggttgaag aaaattcttggattctgag	180
agtctccgtt agactgtttc acagaaggat gtgtgtgtac ccaaggctac acatcaaaaa	240
gaaatggata aaataagtgg aaaatttagaa gattcaacta gcctatcaaa aatcttggat	300
acagttcatt cttgtgaaag agcaaggaa cttaaaaaag atcaactgtga acaacgtaca	360
ggaaaaaatgg aacaaatgaa aaagaatgtt tttgtactga aaaagaaaact gtcagaagca	420
aaagaaaataa aatcacagtt agagaaccaa aaagttaaat gggacaaga gctctgcagt	480
gtgagggttc tcacactcat gaaaatgaaa attatcttt acatgaaaat tgcatgttga	540
aaaaggaaaat tgccatgcta aaactggaaa tagccacact gaaacaccaa taccaggaaa	600
aggaaaataa atacttttag gacattaaga tttttaaaaga aaagaatgct gaacttcaga	660
tgaccctaaa actgaagag gaatcattaa ctaaaaggcc atctcaatat agtggcagc	720
ttaaagttct gatagctgag aacacaatgc tcacttctaa attgaaggaa aaacaagaca	780
aagaaaataact agaggcagaa attgaatcac accatccatg actggcttct gctgtacaag	840
accatgatca aattgtgaca tcaagaaaaa gtcaagaacc tgcttccac attgcaggag	900
atgcttggttt gcaaagaaaa atgaatgtt atgtgagtag tacgatatat aacaatgagg	960
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aacgtgaaac acagtgtcaa atgaagggaa ctgaacacat gtatcaaaaac gaacaagata	1140
atgtgaacaa acacactgaa cagcaggagt ctctagatca gaaatttattt caactacaaa	1200
gcaaaaaatgtt gttggctcaa cagaattag ttcatgcaca taagaaaagct gacaacaaaa	1260
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tttcatgattt cttccrtaag cctggggcgcac agagcgcagac ttgtctcaa aaaaaaaaaa	1620
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<210> 179

<211> 179

<212> PRT

<213> Homo sapien

<400> 179

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Asn Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser Lys	
35 40 45	
Gln Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu	
50 55 60	
Thr Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln Lys	
65 70 75 80	
Glu Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser	
85 90 95	
Lys Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln	
100 105 110	
Lys Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys	
115 120 125	

Lys Phe Cys Val Leu Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys
 130 135 140
 Ser Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser
 145 150 155 160
 Val Arg Phe Leu Thr Leu Met Lys Met Lys Ile Ile Ser Tyr Met Lys
 165 170 175
 Ile Ala Cys

<210> 180
 <211> 1681
 <212> DNA
 <213> Homo sapien

<400> 180

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 caaaaagaaaat aaaatcacag ttagagaacc aaaaagttaa atggaaacaa gagctctgca 180
 gtgtgagatt gactttaaac caagaagaag agaagagaag aaatgccat atattaaatg 240
 aaaaattag ggaagaatta ggaagaatcg aagagcagca tagggaaagag tttagaagtga 300
 aacaacaact tgaacaggct ctcaaatc aagatataga attgaagagt gtagaaagta 360
 atttgaatca ggttctcac actcatgaaa atgaaaattta tctcttacat gaaaattgca 420
 tggaaaaaa gggaaattgcc atgctaaaac tggaaatagc cacactgaaa caccaatacc 480
 agaaaaagga aaataaatac tttgaggaca ttaagatttt aaaaagaaaag aatgctgaaac 540
 ttccatgtac cctaaaactg aaagaggaat cattaactaa aaggccatct caatatagtg 600
 ggcagctaa agttctgata gctgagaaca caatgctcac ttctaaattt aaggaaaaac 660
 aagacaaaga aatactagag gcagaaattt aatcacacca tccttagactg gcttctgctg 720
 tacaagacca tgatcaaatt gtgacatcaa gaaaaagtca agaacatgtct ttccacattt 780
 caggagatgc ttgtttgcaa agaaaaatgt atggttgcattt gaggatgtc atatataaca 840
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<210> 181
 <211> 432
 <212> PRT
 <213> Homo sapien

<400> 181

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Val Leu Lys Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu
35 40 45
Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val Arg Leu
50 55 60
Thr Leu Asn Gln Glu Glu Lys Arg Arg Asn Ala Asp Ile Leu Asn
65 70 75 80
Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His Arg Lys
85 90 95
Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile Gln Asp
100 105 110
Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser His Thr
115 120 125
His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu Lys Lys
130 135 140
Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His Gln Tyr
145 150 155 160
Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu Lys Glu
165 170 175
Lys Asn Ala Glu Leu Gln Met Thr Leu Lys Leu Lys Glu Glu Ser Leu
180 185 190
Thr Lys Arg Ala Ser Gln Tyr Ser Gly Gln Leu Lys Val Leu Ile Ala
195 200 205
Glu Asn Thr Met Leu Thr Ser Lys Leu Lys Glu Lys Gln Asp Lys Glu
210 215 220
Ile Leu Glu Ala Glu Ile Glu Ser His His Pro Arg Leu Ala Ser Ala
225 230 235 240
Val Gln Asp His Asp Gln Ile Val Thr Ser Arg Lys Ser Gln Glu Pro
245 250 255
Ala Phe His Ile Ala Gly Asp Ala Cys Leu Gln Arg Lys Met Asn Val
260 265 270
Asp Val Ser Ser Thr Ile Tyr Asn Asn Glu Val Leu His Gln Pro Leu
275 280 285
Ser Glu Ala Gln Arg Lys Ser Lys Ser Leu Lys Ile Asn Leu Asn Tyr
290 295 300
Ala Gly Asp Ala Leu Arg Glu Asn Thr Leu Val Ser Glu His Ala Gln
305 310 315 320
Arg Asp Gln Arg Glu Thr Gln Cys Gln Met Lys Glu Ala Glu His Met
325 330 335
Tyr Gln Asn Glu Gln Asp Asn Val Asn Lys His Thr Glu Gln Glu
340 345 350
Ser Leu Asp Gln Lys Leu Phe Gln Leu Gln Ser Lys Asn Met Trp Leu
355 360 365
Gln Gln Gln Leu Val His Ala His Lys Lys Ala Asp Asn Lys Ser Lys
370 375 380
Ile Thr Ile Asp Ile His Phe Leu Glu Arg Lys Met Gln His His Leu
385 390 395 400
Leu Lys Glu Lys Asn Glu Glu Ile Phe Asn Tyr Asn Asn His Leu Lys
405 410 415
Asn Arg Ile Tyr Gln Tyr Glu Lys Glu Lys Ala Glu Thr Glu Asn Ser
420 425 430

<210> 182

<211> 511

<212> DNA

<213> Homo sapiens

<400> 182
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cattatcttt gagtctatat tctcttggc tgtaagaaga tgaggaatgt aataggctg 180
ccccaaaggct ttcatgcctt ctgtaccaag cttgtttcct tgcataatc tccaggctc 240
tggctgcccc ttatggaga atgtgatttc caagacaatc aatccacaag tgtctaagac 300
tgaatacaaa gaacttcttc aagagttcat agacgacaat gccactacaa atgccataga 360
tgaattgaag gaatgtttc ttaaccaaac ggatgaaact ctgagcaatg ttgaggtgtt 420
tatgcaatta atatatgaca gcagtcttg tgatttattt taacttctg caagaccctt 480
ggctcacaga actgcagggt atggtgagaa a 511

<210> 183
<211> 260
<212> DNA
<213> Homo sapiens

<400> 183
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gccagggtgca gcgtccatct ccacattgac atctccaccc acctggcctc tcagggcatt 180
catctctcc tcgtggttct tcttcaggta gcccagctcc tccttcaggc tctcaatctg 240
catctccagg tcagctctgg 260

<210> 184
<211> 461
<212> DNA
<213> Homo sapiens

<400> 184
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ctctatTTTA gatagattaa cattaaccaa cataatTTTT ttttagatcga gtcaGcataa 180
atttctaagt cagcctctag tcgtggttca tctcttccac ctgcatttttta tttgggtttt 240
gtctgaagaa aggaaaagagg aaagcaaaata cgaattgtac tatttttacc aaatctttgg 300
gattcattgg caaataattt cagttgtggt tattttaaa tagaaaaaaaaaaatTTTGTt 360
tccttaggttgg aaggtctaat tgataccgtt tgactttaga tgaccatTTA tgactttca 420
aatgaatttgc ttccaaaat aaatgaagag cagacctcgg c 461

<210> 185
<211> 531
<212> DNA
<213> Homo sapiens

<400> 185
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caggcagtga acttgacatg attagctggc atgattttttt ctttttttcc ccccaaaacat 120
tgtttttgtg gccttgaatt ttaagacaaa tattctacac ggcatttgc acaggatgg 180
tggaaaaaaa aagtttaaaa acaaaaaccc ttaacggAAC tgcctaaaaa aggccagacgt 240
cctagtgcct gtcatttat attaaacata catacacaca atcttttgc ttattataat 300
acagacttaa atgtacaag atgtttcca ctttttcaaa ttTTTAAACA caacagctat 360
aaacctgaac acatatgcta tcattcatgcc ataagactaa aacaattata ttttagcgaca 420
agttagaaagg attaaatagt caaatacaag aatgaaaaac gcagtacata gtgtcgca 480
ctcaaatcggtt catttagata gatccagggtt tttaaacggc acgttttgc t 540

<210> 186
<211> 441
<212> DNA
<213> Homo sapiens

<400> 186
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atcaaaagaa tcatcatctt taccttactt ttcaggaa ttactgaact ttcttcttag 120
aagataggc acagccattt ccttggctc acttgaaggg tctgcattt ggtcctctgg 180
tctcttgcca agtttccaa ccactcgagg gagaataatc gggagggtt acttcctccg 240
gggcttcccc gagggcttca ccgtgagccc tgcggccctc agggctgcaa tcctggattc 300
aatgtctgaa acctcgctt ctgcctgctg gacttctgag gccgtcaactg ccactctgtc 360
ctccagctct gacagcttcatctgtt cctgttgcac tggacgggtt cccagggtc 420
ctgggggctt tttcctgtc t 441

<210> 187
<211> 371
<212> DNA
<213> Homo sapiens

<400> 187
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caggctgctg atggtagag tgaactctgt cccagatcca ctgcccctga accttgcattg 120
gaccggat tctaaaacttag acgccttatg gatcaggagc tttggggctt tccctggttt 180
ctgttgcatac caggccaaacc aactactaac actctgactg gcccccaag tgatgggtac 240
tctgtctccct acagttgcag acagggtgga aggagactgg gtcatctgga tgtcacatattt 300
ggcacctggg agccagagca gcaggagccc caggagctga gcggggaccc tcatgtccat 360
gctgagtccct g 371

<210> 188
<211> 226
<212> DNA
<213> Homo sapiens

<400> 188
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tttatttctt tgatattttt cttttttttt tttttgttgg tggggacttg tgaatttttc 120
taaagggtctt atttAACATG ggaggagagc gtgtgcggct ccagcccaac ccgtgtctca 180
cttccacccc tctctccacc tgcctctggc ttctcaggac ctgccc 226

<210> 189
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(391)
<223> n=A,T,C or G

<400> 189
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cctcggccgc naccacgcta agggcgaatt ctgcanatat ccatcacact ggcggccgt 180
cgagcatgca tctanagggc ccaattcncc ctatagttag ncgttattaca attcactggc 240

cgtcgaaaaa caacgtcgatg actggaaaaa ccctggcggtt acccaactta atgcgcattgc 300
agcacatccc ccttcncca gctggctaa tancgaagag gcccgacccg atcgcccttc 360
ccaacanttg cgcaagcctga atggcgaatg g 391

<210> 190
<211> 501
<212> DNA
<213> Homo sapiens

<400> 190
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actggaggag ctggcagagg cgttgctgtc aaactcctct gccacatctt cctcccttc 120
acctgggttg aatgactcat cggtttcttc ttctgagtca tcgctgtgtt catggcatt 180
ctcctcccg atcttgcctt ctccttcat cctctccaag taggcattcat gctggccttc 240
atcagagtca gcatattcat ctagcttgg gttcatgccc tctttcaatc ctgggtttt 300
gatgttgcgt tttttcggt tgacaaaatc aaacagtttcccgtaacttccctt ccctctcaat 360
gctgctgaag gtataactgag tgccctgctt ggtctcaatt tcaaagtcaa aggaacgagt 420
agtagtggta ccacgagcaa agttgacaaa ggagatctca tcgaagcggg tgcacacagg 480
tggcttgcgtt acgttagatga a 501

<210> 191
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (49)
<223> n=A,T,C or G

<400> 191
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aacagaaaatg aaaaactaac atggattgct ataaatatgc tgaagcttag ttgttcaat 120
gatacaattc tctcatgcta ctctaaagtt tataaaagaaa aaggatttac actttacaca 180
ctgtacaccaa aaggaataacc ttctgagagc cagggagtgg ggaaaggggg aggagacttg 240
a 241

<210> 192
<211> 271
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(271)
<223> n=A,T,C or G

<400> 192
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gatagaagan caaaccacgt cccacgaatc ccaataatga cagtttcaga ctttgctttt 120
ttaacaattt gaaaaattat tcttaatgt ataaagtaat ttatgtaaa ttaataaaatc 180
ataatttcattt ttccacattt attaaagctg ctgtatagat tttagggngca ggacttaata 240
atagnngaaa tgaaaattatg atttattaat c 271

<210> 193

<211> 351
<212> DNA
<213> Homo sapiens

<400> 193
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taacttcctg tgcccttcct atcacctcga gaagtaatta tcagttgggt tggatttttg 120
gaccaccgtt cagtcattt gggtgtccgt gctcccaaaa cattttaaat gaaagtattt 180
gcattcaaaa agacagcaga caaaatgaaa gaaaatgaga gcagaaagta agcatttcca 240
gcctatctaa ttcttttagt ttcttatttg cctccagtgc agtccatttc ctaatgtata 300
ccagcctact gtactatcta aaatgctcaa ttccagcacc gatggacctg c 360

<210> 194
<211> 311
<212> DNA
<213> Homo sapiens

<400> 194
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caccctccct ctgctggat gaggtccagg agccaactaa aacaatggca gaggagacat 120
ctctgggttt cccaccaccc tagataaaaa tccacagcac agaccttac cggtttctc 180
ttccatccct aaaccacttc cttaaatgt ttggatttgc aaagccaatt tggggcctgt 240
ggagcctggg gttggatagg gccatggctg gtcccccacc ataccccccc tccacatcac 300
tgacacagac c 311

<210> 195
<211> 381
<212> DNA
<213> Homo sapiens

<400> 195
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gccaacagga tgacatgaaa tgatgtactc agaagtgtcc tggaatgggg cccatgagat 120
gggtgtctga gagagagctt cttgtctgt cttttcctt ccaatcaggg gctcgctctt 180
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aatagtagcc tctgtgacac caggcgaaaa ccgaggacc acttctctgg gaggagaccc 300
aggcttctca tacttgatga tgtagccgtt aatcctggca cgtggggct gccatgatac 360
cagcaggaa ttgggtgtgg t 381

<210> 196
<211> 401
<212> DNA
<213> Homo sapiens

<400> 196
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gccccaaacctt ggagacctga ttgagatttt ccgccttggc tatgagact gggccctgtt 120
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tattgtgagc aggaactgtg agcactttgt caccctgacc t 401

<210> 197
<211> 471

<212> DNA

<213> Homo sapiens

<400> 197

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 aactttgtac cttgattgcc ttacaaaagg atttgttac aaacagcgac catataaaag 120
 cctcctgccc caaagcttgt gggcacatgg gcacatacag actcacatac agacacacac 180
 atatatgtac agacatgtac ttcacacac acaggccaca gcatacacac gttttcttag 240
 gtacagctcc caggaacagc taggtgggaa agtcccatca ctgagggagc ctaaccatgt 300
 ccctgaacaa aaattgggca ctcatctatt cttttctct tggtcccta ctcattgaaa 360
 ccaaactctg gaaaggaccc aatgtaccag tatttatacc tctagtgaag cacagagaga 420
 ggaagagagc tgcttaaact cacacaacaa tgaactgcag acacagacct g 480

<210> 198

<211> 201

<212> DNA

<213> Homo sapiens

<400> 198

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tggcctatgc agtcaactcc tggaccacta gtatttcagg tatgctgctg aaagtggaa 180  
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<210> 199

<211> 551

<212> DNA

<213> Homo sapiens

<400> 199

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gggtggccccc tgaccttatt actgtcattt agtcccttga ccttgccact tcaatccctgg 480
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<210> 200

<211> 211

<212> DNA

<213> Homo sapiens

E2203

<221> misc feature

<222> misc_feature

<223> B=A T C or G

<400> 300

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<210> 201
<211> 111
<212> DNA
<213> Homo sapiens

<400> 201
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<210> 202
<211> 331
<212> DNA
<213> Homo sapiens

<400> 202
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ctcaaattgtat gcttttaagg gaggacagtgc gataaaaata aactttttt ttctccctac 180
aatacataga agggttatca aaccactcaa gtttcaaaat ctttccaggg tccaatatca 240
ctttttttctt ttcggttcaa tgaaaagcta aatgtataaa tactaattt agataaaaatt 300
ttatTTTact tttaaaaat ttgtccagac c 331

<210> 203
<211> 491
<212> DNA
<213> Homo sapiens

<400> 203
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ggaaaggtagtgc gatggctta agttagtgc atgtataggt tagggatctt ttggttttaa 180
atcacagaaaa acctaatac aactggctta aaataaaaag gatttattgg ttcatgtaaac 240
tagaaaagtcc ataggttagtgc ctggctccag gtgaagactt gacccagtag ttcatgtatgt 300
ctctaaatac cggactgact ttttctcact tggatcttgc tctgttaggac cattaaatgc 360
tggccactt aatggctgccc agcatttcttca agattacact tttccccatt tatgtccaaat 420
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<210> 204
<211> 361
<212> DNA
<213> Homo sapiens

<400> 204
tcccttcctc ccccatgtga taaatgggtc cagggtcgat caaaagaactc tgactgcaga 60
actgcccgtc tcagtggaca gggcatctgt tattcctgaga cctgtggcgac acacgtcttg 120
ttttcatttg atttttgtta agagtgcaatg attgcagatg cttagagaaat ttttgtttcc 180
ttgattaaca tgatTTTctt ggTTTttaca tccagggcat ggcagttggcc tcagccttaa 240
acttttggtc ctactccac cctcagcgaa ctggggcagca cggggagggt ttggctaccc 300
ctgccccatcc ctgagccagg taccaccatt gtaaggaaac actttcagaa attcagacct 360
c 361

<210> 205

<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (2)
<223> n=A,T,C or G
<221> misc_feature
<222> (3)
<223> n=A,T,C or G

<400> 205
cnngtacagt tcttcctgga tggccgacac agatcctggg gaaaggcaat cctggcactg 60
ctctgaaacc agagtcctc ctcctcccc gggcagggtg gagctgagaa gggctgcct 120
agcgttggga ctccacctcc atacacctga tattttgata gggcagggtcc ctgctatggg 180
ccactgttct gggcagtata gtatgcttga cagcatcctt ggcatctatc caccagatcc 240
cagagcaccc gctactagct gtgacaacat cctccaaaaca ttgcaaaatt tcccctggga 300
ggcaagattg cctcagatgg gagaatcacg ctcttagggaa atctgctggg atgagaaccc 360
caactcccca ctccactgag cttccagatg gcgagcaggc tgcaagctcca gcacagacac 420
gaagctccct ccagccactg acggtccatg gctggggta cccaggacac c 480

<210> 206
<211> 261
<212> DNA
<213> Homo sapiens

<400> 206
tagagtattt agagtcctga gataacaagg aatccaggca tccttttagac agtcttcgt 60
tgtccttct tcccaatcag agatttggg atgttgaaa tgacaccacc accagcaatt 120
gtagccttga tgagagaatc caatttctca tctccacgaa tagcaagttg caagtgacga 180
ggggtaataac gcttacctt taagtctttt gatgcatttc ctgccagttc aagtacctct 240
gcggtgaggt actccaggat g 261

<210> 207
<211> 361
<212> DNA
<213> Homo sapiens

<400> 207
gctctccggg agcttgaaga agaaactggc tacaaagggg acattgccga atgttctcca 60
gcggtgttta tggacccagg cttgtcaaac tgtactatac acatcgtgac agtcaccatt 120
aacggagatg atgcccaaaa cgcaaggccc aagccaaagc caggggatgg agagttgtg 180
gaagtcattt ctttacccaa gaatgacctg ctgcagagac ttgatgctct ggtagctgaa 240
gaacatctca cagtggacgc cagggtctat tcctacgctc tagcactgaa acatgcaaatt 300
gcaaagccat ttgaagtgcc cttcttgaaa ttttaagccc aaatatgaca ctggacctgc 360
c 361

<210> 208
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (1) ... (381)
<223> n=A,T,C or G

<400> 208
agaggagatn ttgccatgc ctgaatnctt tcctatncca ccctancact taacatatta 60
cttagtctgc tttgntaaaa gcaagtatta ccttnaactt gnctcttaact ctttgccctt 120
tagctaacta ataaagnnttg atntaggcat tattatataa ttctgagtc ttcatggtat 180
ctctcatgtt tgatgtatTT tncaaactaa gatctatgat agttttttt ccanagttcc 240
attaaatcat ttatTCCTT tacttctca cctctgtnga aacatttaga aactggattt 300
gggaacccan ttttggaaaa ccagattcat agtcatgaaa atggaaactt ncatattctg 360
ttttgaaaa gatgtggacc t 381

<210> 209
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (83)
<223> n=A,T,C or G

<400> 209
gtggagagca agtgatttat taaagcaaga cgttgaaacc tttacattct gcagtgaaga 60
tcagggtgtc attgaaagac agngaaacc aggtgaaag tttttacatg tcacacacta 120
catttcttca atatTTcac caggacttcc gcaatgaggc ttctgttctg aaggggacatc 180
tgatccgtgc atctttcac tcctaacttg gctgcaacag cttccacctg c 240

<210> 210
<211> 371
<212> DNA
<213> Homo sapiens

<400> 210
tccatcctgg ttttgcagag atcaggttgt tgacagttcc tggttgaccc acagctaccc 60
atgtcagtttca tctccactaa catatccaag aatctttgtt ggacaatttc tccacctgca 120
agtttttta ggtagaactc ttcttttaag gcaatttagcc cattgcctaa aggtttact 180
gtcttaaagc tgtctttctg agatctaatt ccaaggactt ctccacagct aagtggatg 240
cctcacacca ttaggtgtatg ctggacag aacagagtat ttcatcttg tggtaaagc 300
aatttccttgg cttcggtcc tcaccacttt ctatgccagt ctcccattha tggccctagt 360
aatgcctatg c 371

<210> 211
<211> 471
<212> DNA
<213> Homo sapiens

<400> 211
tttattttaa aaaaaaaaaa ttaaaataga gccaacaaat gcaattaaga aaaaaaaaaagt 60
attgagacac aaggggacct acatgttctg gtctaaagaag catgcaagta ttacaaagca 120
ttccagatac agtatgacag aggaacagtg aacaaggattt ggaacgtgc tcttttttc 180
agaaacggga agtctaacag ttatgtttc acaatggtag tgattaaacc atctttatTT 240
ttaaggaatt ttatggaaag aatttttagca ccatcattaa aggaaaaata ataataccctt 300
tttagccctg cctatctcca gtcttggaat aataacagaa gcatagcacc ttctcagtatc 360
taaaatataa acaagaatag taagtccatc ccagcttcta gagatgaggt agctcatgct 420

aagaaaatgtt gggtcatttt tcctatgaaa gttcaaaggc caaatggtca c 480
<210> 212
<211> 401
<212> DNA
<213> Homo sapiens

<400> 212
tggcctgtct cttcacata gtccatatca ccacaaatca cacaacaaaa gggagaggat 60
atattttggg ttcaaaaaaa gtaaaaagat aatgttagctg catttttttg gttattttgg 120
gccccaata tttcctcatc tttttgttgt tgtcatggat ggtggtgaca tggacttg 180
tatagaggac aggtcagctc tctggctcggt tgatctacat tctgaagttg tctgaaaatg 240
tcttcatgtat taaattcagc ctaaacgttt tgccgggaac actgcagaga caatgctgtg 300
agtttccaac ctccatgtt ctgcgggcag agaaggctta gtttgcacat caccattatg 360
atatcaggac tggttacttg gtttaaggagg ggtctacctc g 401

<210> 213
<211> 461
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(461)
<223> n=A,T,C or G

<400> 213
tgtgaagcat acataaaataa atgaagtaag ccatactgat ttaatttttattt ggttgttattt 60
ttcccttaaga cctgaaaaatg aacatagtat gctagttattt tttcagtgtt agcccttttac 120
tttcctcaca caatttgaa tcatataata taggtactttt gtcctgtt aaataatgtg 180
acggatagaa tgcatcaagt gtttattatg aaaagagtgg aaaagtatat agcttttanc 240
aaaaggtgtt tgcccattct aagaaatgag cgaatatata gaaatagtgn gggcatttct 300
tctgtttagg tggagtgtat gtgttgacat ttctccccat ctcttccac tctgtttnt 360
ccccattatt tgaataaagt gactgctgaa nangactttg aatccttatac cacttaattt 420
aatgtttaaa gaaaaaccta taatggaaag tgagactcct t 461

<210> 214
<211> 181
<212> DNA
<213> Homo sapiens

<400> 214
cctgagcttc tactccttcc ccttaagatt cctccaaagc accagctcca taaaatcctt 60
cagctccccca gacccacacc aagaacccca catgttaattt ggatcagcca aatctacaag 120
cagataagtc ctaaggagaa tgccgaagcg tttttcttct tcctcaagcc tagcatgaga 180
c 181

<210> 215
<211> 581
<212> DNA
<213> Homo sapiens

<400> 215
ctgctttaag aatggtttcc cacctttcc ccctaattctc taccaatcag acacattttta 60
ttatTTTaaat ctgcacccctt ctctatTTTta tttgccagg gcacgatgtg acatatctgc 120

agtcccagca cagtgggaca aaaagaattt agacccaaa agtgtcctcg gcatggatct 180
 tgaacagaac cagtatctgt catggaactg aacattcatc gatggctcc atgtattcat 240
 ttattcactt gttcattcaa gtatttattt aatacctgcc tcaagctaga gagaaaaagag 300
 agtgcgctt ggaaattttt tccagtttc agcctacage agattatcg ctcggtgact 360
 tttcttctg ccaccattn ggtgatggtg tttgattcag agatggctga atttctattc 420
 ttagcttatt gtgactgttt cagatctagt ttggaaacag attagaggcc attgtcctct 480
 gtcctgatca ggtggctgg ctgtttctt ggatccctt gtcggcggc caccggcggc 540
 cctgactctt gagaatcaag aaaacaccca gaaaggacct c 581

<210> 216
 <211> 281
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(281)
 <223> n=A,T,C or G

<400> 216
 ccgatgtcct gcttctgtgg accagggct cctctgnngg tggcctcaac cacggctgag 60
 atccctagaa gtccaggagc tgtgggaaag agaagcactt agggccagcc agccggcac 120
 ccccaattgc gccccgaccc acgctcacgc accagacctg cccngcggg cgtcnnaag 180
 ggcgaattct gcagatatcc atcacactgg cggacgctcg agcatgcata tagagggccc 240
 aattcaccct atantgagtc gtattacaat tcactggccg t 281

<210> 217
 <211> 356
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(356)
 <223> n=A,T,C or G

<400> 217
 atagcaggtt tcaacaattt tctttagtt tgnagtaaaa agacataaga aagagaagg 60
 gtgtttgca gcaatccgtt gttggtttctt caccataccc tgcatgttc tgagccaaag 120
 gtcttgcaga aagttaaaaat aaatcacaaa gactgctgtc atatattaat tgcataaaaca 180
 cctcaacatt gctcagagg tcatccgtt gtttaagaaa acattccctt aattcatcta 240
 tggcatttg agtggcatgt tcgtctatga actcttgaag aagttttt tattcagtct 300
 tagacacttg tggattgatt gncttggaaa tcacattctc caataaggga cctcgg 360

<210> 218
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 218
 ttgtccatcg ggagaaaagg gtttgcagt tgtttctata accagattga ggaggacaaa 60
 ctgctctgcc aatttctgaa tttcttttattt ttcagcaaac actttcttta aagcttgact 120
 gtgtggcac tcatccaagt gatgataat catcaagggt ttgttgcgt tgctggattt 180
 atatacgtt tcttcatatg tctgagtcac gatgagttgg tcaccccaac ctctggagag 240
 ggtctggggc agtttgggtc gagatccctt tttgtccctt tggtccctt gtttgcgtt 300

ggtatctctg gacctgcctg g 321

<210> 219
<211> 271
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (41)
<223> n=A,T,C or G

<400> 219
ccggtaggt ccacgcgggg gcagtgagg cacaggctca ngtggccgg gctacctggc 60
accctatggc ttacaaaga gagttggccc agtttccctc cacctgaggg gagactctg 120
actcctaaca gtcttcctg ccctgccatc atctgggtg gctggctgtc aagaaaaggcc 180
ggccatgctt tctaaacaca gccacaggag gctttaggg catcttccag gtggggaaac 240
agtcttagat aagtaaggtg acttgtctaa g 271

<210> 220
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(351)
<223> n=A,T,C or G

<400> 220
gtctacgac gaggaccagc ttttcttctt cnactttcc canaacactc ggggcctcg 60
cctggccgaa tttgctact gggctcagga acagggagat gtcctgcctt ttttatttga 120
caaagagttc tgcgagtgta tgatccagca aatagggcca aaacttcatg ggaaaatccc 180
ggtgtccaga gggtttccctt tcgctgaatgt gttcacgcgtc aagccccctgg agtttggcaa 240
gccaacact ttgtctgtt ttgtcagtaa tctttccca cccatgtca cagtgaactg 300
gtacatcat tccgtccctg tggaaaggatt tgggcctact ttgtctcag a 360

<210> 221
<211> 371
<212> DNA
<213> Homo sapiens

<400> 221
gtctgcagaa gcgtgtctga ggtgtccgggt ggaggtggca gcccagctct gggactaatac 60
accgtgtgg ggacggcacc gcgtcaggat gcaggcagat ccctgcagaa gtgtctaaaa 120
ttcacactcc tcttctggag ggacgtcgat ggtatttagga tagaagcacc aggggacccc 180
acgaacgggtg tcgtcgaaac agcagccctt attgcacac tgggaggcg tgacaccagg 240
aaaaccacaa ttctgtcttt cacggggggc cactgtacac gtctctgtct gggcctcgcc 300
cagggtgccg agggccagca tggacaccag gaccaggcg cagatcacct ttttctccat 360
ggtgaccc 371

<210> 222
<211> 471
<212> DNA
<213> Homo sapiens

<400> 222
gtccatgttc catcatataat gttccaacat caccaggac acaaagctgc aaaaatgaga 60
aggaaataa ggtagagaa aggatccggg caatcttaag gactgagggaa gacatgtcc 120
ccaaaccttg aactcacaaa ccctgaagct caaggattgc atccttcctc caaatctcac 180
tcaacataat aagtgcagaa caacatgcc aagcactgt a tgaagcacta gggacaaaga 240
caaggtcaaa atccttgtaa ccaaatttaa tggattgt a tgcagtgtt aacacaggac 300
agtaacagaa caccctaaagaa ccaaaccagaa gagggtaggg ataagcataa atgaagtaac 360
atgaaataaa ctccaaatg gaaaacttgt ccatcccccc agggcaagtc aactacagtc 420
tcccaaagga cataaaattcc acttagggca cactagacag aaaacaatat t 480

<210> 223
<211> 411
<212> DNA
<213> Homo sapiens

<400> 223
agttgctcta caatgacaca caaatcccgt taaataaaatt ataaacaagg gtcaattcaa 60
atgtgaagta atgttttagt aaggagagat tagaagacaa caggcatagc aaatgacata 120
agctaccgat taactaatcg gaacatgtaa aacagttaca aaaataaaacg aactcttcctc 180
ttgtcctaca atgaaagccc tcatgtgcag tagagatgca gtttcatcaa agaacaaaca 240
tccttgc当地 tgggtgtgac gcgggtccag atgtggattt ggcaaaacct catttaagta 300
aaaggttagc agagcaaagt gcgggtctt agctgtgtc tgcgtcgctg tggcgtcggg 360
gaggctctc cttcccccagc tttgtgcct gagaggaacc a 420

<210> 224
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (31)
<223> n=A,T,C or G

<400> 224
ggctgaagt ttgataacaa agaaatataat ntaagacaaa aatagacaag agttaacaat 60
aaaaacacaa ctatctgtg acataacata tggaaacttt ttgtcagaaa gctacatctt 120
cttaatctga ttgtccaaat cattaaaata tggatgattc agtgcctt tgccagaaaat 180
tcgtttggct ggatcataga ttaacatttt cgagagcaaa tccaagccat tttcatccaa 240
gttttgaca tggatgcta ggctcctgg tttccatgg ggaaatgtat tcttatagtc 300
ctgtaaagat tccacttctg g 321

<210> 225
<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (34)
<223> n=A,T,C or G

<400> 225
atgtctgggg aaagagttca ttggcaaaag tgnctccca agaatggttt acaccaagca 60

gagaggacat gtcactgaat gggaaaagg aaccccgta tccacagtca ctgtaaagcat 120
ccagtaggca ggaagatggc tttgggcagt ggctggatga aagcagattt gagataaccca 180
gctccggAAC gaggtcatct tctacaggtt cttccttcac tgagacaatg aattcagggt 240
gatcatttctc t 251

<210> 226
<211> 331
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (1)...(331)
<223> n=A,T,C or G

<400> 226
gttaggtccc aggccccccg ccaagnggtt accnnnnntna ccactcctga cccaaaaatc 60
aggcatggca taaaacgtt gcaaattccct ttactgttat cccccccacc accaggacca 120
tgttagggtgc agtctttact ccctaaccgg tttcccgaaa aaggtgtcac ctcccttcca 180
gacagatgag agagggcagg acttcaggct ggatccacca ctgggctctc cctcccccag 240
cctggagcac gggaggggag gtgacggctg gtgactgatg gatgggtagt gggctgagaa 300
gaggggacta ggaagggcta ttccaggctc a 331

<210> 227
<211> 391
<212> DNA
<213> Homo sapiens

<400> 227
aggctgtccc ttgaagtata ggaaggaatc atagttggag gacttctgca ttatgttg 60
gctgaagcta gaagtgcac cccctcctga tttctgcagc aagatgaact gccttatccc 120
cagccccgcag gaatgttcat atctgagcaa tcaatggca ctgtgttcaa ccacgccatt 180
ttcaagattt gctccttaaa ccaccacaa ggcaccagct ctgggagaag ctgcagggag 240
aagagaacaa agccctcgct gtgatcagga tgggtgtctc ataccttttc tctgggtca 300
ttccaggtat gagacagagt tgaacctgctg catgagcgtg gaggccgaca tcaacggcct 360
gcgcagggtg ctggatgagc tgaccctgga c 391

<210> 228
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (35)
<223> n=A,T,C or G

<400> 228
gttgtccata gccacctctt gggatagaag ctttnttagtt catagttcga ttagtgtgtc 60
cttaggacat aggtccagcc ctacagatta gctgggtgaa gaaggcaagt gtctcgacag 120
ggcttagtct ccaccctcag gcatggAAC attcagggtg aagcctggta tggggcaca 180
ggagactcag gctgatataa aaataacaaa atcagtaata aaaaaattat aaaacctgtt 240
gcttgtctga atagatttga gcaacagtct tgctttgtt aaaatcctgg agccgttaag 300
tcctgaatat tcttctggac atcattgtcg gctggagaaa ggagcccccag gcccggctcg 360
gtgacatct gtcaggtttg gaagtctcat c 391

<210> 229
<211> 341
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (202)
<223> n=A,T,C or G

<400> 229
gtccatggct tctcaccagg acagtctttc tgggcaactt ggggaagccc ctgttctgct 60
caagtctcac cccatggaaag aggtggggga agggggccctt ggaaaaatcg gaagacgggt 120
tggagagcac gagtcactac aaagcagtaa aagtgaatgg tgtctccagg ggctgggtcc 180
agaacaccgc ggagagcccc anccataaaag gtgtgttccg cctctggct gcaggaatct 240
cttgaatct ctttgatgg tggctccaag agcaatggga agtcaacagc caggaggctg 300
gactgggttc cctgggaccc cgaggtccca gaggctgctg g 341

<210> 230
<211> 511
<212> DNA
<213> Homo sapiens

<400> 230
gtccaaggcca aggaaaccat tcccttacag gagacctccc tgtacacaca ggaccgcctg 60
gggctaaagg aaatggacaa tgcaggacag ctgtgtttc tggctacaga aggggaccat 120
cttcagttgt ctgaagaatg gtttatgcc cacatcatac cattccttgg atgaaaacccg 180
tatagttac aatagagtc agggagcccc taactcttcc aaaccacatg ggagacagtt 240
tccctcatgc ccaaggctga gctcagatcc agcttgcac taatccttct atcatctaac 300
atggcctact tggaaagatc taagatctga atcttattcct ttgccatctt ctgttaccat 360
atggtgttga atgcaagttt aattaccatg gagattgtt tacaaacttt tgatgtggtc 420
aagttcagtt ttagaaaagg gagtctgttc cagatcagt ccagaactgt gcccaggccc 480
aaaggagaca actaactaaa gtatgagat a 511

<210> 231
<211> 311
<212> DNA
<213> Homo sapiens

<400> 231
ggtccaagta agctgtgggc aggcaagccc ttgggtcacc tggtggctac acagaccct 60
ccccctcggt cagctcaggc agctcgaggc ccccgaccaa cacttgcagg ggccctgct 120
agttagcgcc ccaccgcccgt ggagttcgta ccgtttccctt agaacttcta cagaagccaa 180
gctccctgga gcccgttgg cagctctagc tttgcagtcg tgtaattggc ccaagtcatt 240
gtttttctcg ctcactttc caccaagtgt ctagactcat gtgagcctcg tgcatactcc 300
gggggtggacc t 311

<210> 232
<211> 351
<212> DNA
<213> Homo sapiens

<400> 232
tcgttttagct aataatccct tccttgatga tacactccaa cttctgttt ttctttat 60

ctaaaaagcg gttctgtAAC tctcaatCCA gagatgttaa aaatgtttctt aggcacggta 120
tttagtaaattc aagtAAATTt catgtccctt taaaggacaa acttccagAG atttGAATAT 180
aaatTTTtat atgtgttatt gattgtcgTG taacAAatGG cccccacaaa tttagtagctt 240
aaaatAGcat ttatgatGtc actgtttctt ttgccttttC attaatgttc tgtacagacc 300
tatgtAAACA acTTTGTat atgcataTAG gatAGCTTTT ttgagggat a 360

<210> 233
<211> 511
<212> DNA
<213> Homo sapiens

<400> 233
aggTCTGGat gtaaggatgg atgctctcta tacatgctgg gttggggatg ctgggactgc 60
acagCCACCC ccAGTATGCC gctccaggac tctggacta gggcgccaaa gtgtgcaaAT 120
gaaaatacAG gatacccAGG gaACTTTGAA tttcagattG tgAAAAGAAA acaaATCTTg 180
agactCCACa atcacCAAGC taaAGGAAAA agtcaAGCTG ggaACTGCTT agggCAAAGC 240
tgCTTCCCAt tCTATTcaca gTCATCCCCC tgAGGCTCAC ctgcataAGCT gattgCTTCC 300
tttCCCTat CGTTCTGTA AAAATGCAGA CTCACTGAGC cAGACTAAAT tGTGTGTTCA 360
gtggAAggCT gatcaAGAAC tcaaAAGAAt gcaACCTTTt gtctCTTATC tactacaACC 420
aggaAGCCCC cacttaAGGG ttgtcccacc ttactggact gaaccaAGGT acatTTACA 480
cctactgatt gatgtctcat gtccccctaa g 511

<210> 234
<211> 221
<212> DNA
<213> Homo sapiens

<400> 234
caggTCCAGC gaAGGGGCTT catAGGCTAC accaAGCATG tccacATAAC cgAGGAAGCT 60
ctCTCCATCA gcatAGGCCtC cgatGACCAT ggtgttCCAC aaAGGGTTCA tCTTCGAGCG 120
ccggCTGTAC atggccCTGG tcAGCCATGA atGAATAGCT ctAGGACTAT agCTGTGTCC 180
atCTCCCAGA agCTCCTCAT caATCACCAT ctggCCGAGA C 221

<210> 235
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (33)
<223> n=A,T,C or G

<400> 235
ggTCCAAGAA aggGACATCT atgtGAAAGT ganACTGAGA cAGTGTGGT cacAGGTcat 60
gCTGcAGAAAT aatacATTCC cAGGcACTGT cacGTGGGGG ACCCAAGAGG CCCAGGAGT 120
gACCTATAAC CTCTCCAGAA agACCACtCT gtGTGGCATC acAGTCCACa cAGTTAAGG 180
aaATATTTAG ACTTAACAAAT cAGACACCAAG CTCTTACTCA cACTTACACT cacAGCCCAC 240
acACAAGTGT gCAAACATAC acACACATAT atATTCCTG atACATTcat gGAATATCAG 300
AGCCCTGCCc tGAAGTCGTT agtGTCTGT CTCCCCAAAC CGCTGCTCCC acATTGGCTA 360
agCTCCTCA agAGACCTCA g 381

<210> 236
<211> 441
<212> DNA

<213> Homo sapiens

<400> 236

aggccctgtt gcccctttct tttgcccac ttgcattt gggaaatttga atatttaccc 60
aacacctgtt ctgcatttga tatttggaa aataacttgc gctttgatct tataggctca 120
cagatggagg aacgtaccc ttgttcaga tgagatttgc gacttttgag ttgtatgtca 180
aacagcttgc gatttttggg gactactgag agatgataat tgtatttgtc aatatgaga 240
ggacatgaga ttgggtgggc ataggtgtga aatgacatttgc ttggatgtg tttaccctcc 300
aatctcttg ttgaatgttgc tttaaacgt tggtggtggg cctagtggaa ggtgttgaat 360
catgggggttgc gactcttcat aatttgcatttgc ttggatgtg agcaagtcc 420
tgctctgttgc tgacatgttgc g 441

<210> 237

<211> 281

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(281)

<223> n=A,T,C or G

<400> 237

tcctaaaaaa ttagctgacc ttgttaaaaaa tggtggcggtg agcagtataat tattacctat 60
cttttttat tgggtgtgtg ngtgtgtgtt tttaactaat tggctgaaat atctgcctgt 120
ttccctcttt acatttttct tgggttttc ttatatttac tttgtccatc ttgagatcta 180
ctgtaaatgtg aatnttttaa tgaaaacann nccaagttnt actcttactg ggnctgggac 240
atcagatgttgc attgagaggc caacaggttgc gtcttcatgttgc 281

<210> 238

<211> 141

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(141)

<223> n=A,T,C or G

<400> 238

gtctgcctcc tcctactgtt tccctctatn aaaaagcctc cttggcgca gttccctgag 60
ctgtggatt ctgcactgtt gcttnggatt ccctgatatg ttcccttcaa tccactgaga 120
attaaataaa catcgctaaa g 141

<210> 239

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(501)

<223> n=A,T,C or G

<400> 239

aacaatctaa acaaatccct cggttctann atacaatgga ttccccatat tggaggact 60
 ctgangcttt attccccac tatgcntatc ttatcatttt attattatac acacatccat 120
 cctaaactat actaaagccc ttttccatg catggatgga aatggaagat tttttttaa 180
 ctttgtctag aagtcttaat atgggtctgtt gccatgaagg cttgcagaat tgagtccatt 240
 ttctagctgc ctttattcac atagtgtatgg ggtactaaaaa gtactgggtt gactcagaga 300
 gtcgctgtca ttctgtcatt gctgcatac taacactgag caacactctc ccagtgccag 360
 atcccgtgt a tcatccaag aggagcatc atccctttgc tctaattgtc aggaatgtg 420
 cttattagaa aacaaactgc ttgaccagg aacaagtggc tttagcttaag naaacttggc 480
 tttgctcana tccctgatcc t 501

<210> 240
<211> 451
<212> DNA
<213> Homo sapiens

<400> 240
tgcctgaaa ggccattact aatagaaaaca cagcctttcc aatcctctgg aacatattct 60
gtctgggtt ttaatgtctg tggaaaaaaaaa ctaaacaagt ctctgtctca gttaaagagaa 120
atctattgtt ctgaagggtt ctgaacctct ttctgggtct cagcagaagt aactgaagta 180
gatcaggaag gggctgcctc aggaaaaattc cttagatccta ggaattcagt gagaccctgg 240
gaaggaccag catgtaatc agtgcgtatgg aatccacagt ctttacttcc tgctctataa 300
aggccaggt cttcccagta ccaagtcctt tcctcatgaa gttgtgtgc ctcaaggctgt 360
ttagggacca ttgcctgtct tggtcacatg agtctgtctc cttactttag tccctggca 420
atccttgctt aatgcttttg ttgactcaac g 451

<210> 241
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (411)
<223> n=A,T,C or G

<400> 241
aatctccagt gtatggtat cggggtaga gcttcaatct ccagtgtat ggtactgcag 60
cnagagcttc aatctccagt gngatggtat tagggtaga tcttcaatct ccagtgtat 120
ggtatcaggg ttagagcttc agcctccagt gtatggtat cagggtaga gcttcagcct 180
ccagtgtat ggtatcgggg ttagatcttc aatccccagt ggtgggtt agagcttcaa 240
tctccagtgt gatggatgg gggtagagc ttcaatctcc agtctgtatgg tgggggg 300
tggggctttt aagatgtaat tagggttaa gatcataagg gacctgtct gatggggatt 360
agtnccgttn tatgaagaga cacangaggg cttgctctat ctctgactct c 420

<210> 242
<211> 351
<212> DNA
<213> Homo sapiens

<400> 242
ttcccccttca caacagttaga gacctacaca gtgaactttg gggacttctg agatcagcgt 60
cctaccaaga cccccagccca actcaagctt cagcagcaggc acttcccaag cctgctgacc 120
acagtccatcacat cacccatcatcag cacatggaaag gcccctggta tggacactga aaggaagggc 180
tggcctgtcc cttttgaggg ggtgcaaaaca tgactgggac ctaagagccaa gaggtgtgt 240
agaggctcct gctccacactg ccagtctcgta aagaaatggg gttgctgcag tggggatgta 300

ggggcagagg gagggagcca aggtcactcc aataaaacaa gtcatggca c 360
<210> 243
<211> 241
<212> DNA
<213> Homo sapiens

<400> 243
gtctgtgctt tattcaggaaa agcacaagaa tatgtttttc tacctaaaac cctcttctac 60
tttaaaaaatg gtttgctgaa tttttctatg tttttaaaat gtttttatgc ttttttttaa 120
acacgtaaag gatggAACCT aatccctctcc cgagacgcct cttttgtgtt aatgcctatt 180
cttacaacag agaaacaagt acattaatat aaaaacgagt tgattattgg ggtataaaaat 240
a 241

<210> 244
<211> 301
<212> DNA
<213> Homo sapiens

<400> 244
ggtccagagc aatagcgctt gtggtaagc gcctgcactc ctcgggagac atgcctggct 60
tatatgctgc atccacataa ccatagataa aggtgctgcc ggagccacca atggcaaaag 120
gctgtcgagt cagcatttctt cccagggttc catatacctg acctccttca ctttggtccc 180
agccagctac catgagatgt gcagacaagt cctctcgata tttatagctg atatttctca 240
ccacatttgc agcagccaaa acaagtggag gttcctccag ttctatccca tggagctcca 300
g 301

<210> 245
<211> 391
<212> DNA
<213> Homo sapiens

<400> 245
ctgacactgc tgatgtgggc cggggggcgc cgaggcacaa ctggggccg gaccatttag 60
gcacctggag ggtaggcagc ttgtggtgca gacaccacag agagagaaaa gttggatgga 120
gtgggtggaa taatcagggt ggcacactgt gcctagaagc ttccaggggcc accaagagaa 180
tggttggaa aactacaaca ttcacaacag aaataggagt caattcactt agacccagaa 240
ctccagaaag ggggagtgta ggaatctaca atttcaaagc cagctcgtgt ctacctagag 300
ccccaaactg cataagcacc aggattgtac accttagtcc ctcaagatag tttcaagtga 360
gcgtgcaatt cactttaca gaggaggcc t 391

<210> 246
<211> 291
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(291)
<223> n=A,T,C or G

<400> 246
tcctccacag gggaaAGCAGG aagtngacc agttcaggc tggaacgtgc ccagggcaca 60
gagctggcaa ggtgcaaagn cntctgcaga atattcacca ggttgacaca gacctccaca 120
ttcagacata ttccaagctt ctggggctt cagggccccca gaatttcctg gtcttggca 180

tggtnacaaa gtcatttgc cttcctcatt ttggaagggtt ccatttgac ataaaatgca 240
agcgttctcg tgctncatna taataggtcc cagcctgcac tgacacacattt g 300

<210> 247
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(471)
<223> n=A,T,C or G

<400> 247
cactgagtga atgagtatat aatttatgaa aacagaaaaag tgctttggaa aaaaaaaaaag 60
acaacaggag tacatacagn gaaccaaaaa gagtgtacca ggaggagcan accctgaaca 120
gttanaacta tggaaatcgc tatgctttgt gtgtcacag gagttaaaat aggaataaccc 180
tgcataacaat aaatatttat tggataaata actaaggctg atacccttt caatgcgtta 240
tacanactnt atcatcacac cactaatcta agttctcana agttaaacat tacaagactt 300
cagaacaaca taggcgtntt tggctccatt taacanaana aggaccatag tgatcattt 360
atctctatga gtctgtctta tcttctggaa aaggggccta acaccatttc ctittgcaaa 420
aagtagctg ccttgcttcc agttctacca tcctntagca acccatcttt n 480

<210> 248
<211> 551
<212> DNA
<213> Homo sapiens

<400> 248
ccatgggatc aggaatgggg tcaggtcagt tgacctgagc atacccatta aacatgttca 60
aatgtccccca tcccacccac tcacatgaca tggctcccgaa gccctgagat ctgtatccca 120
agaacctcag ttgagaaaata tttatggcag cttcaactgtt gctcaagagc ctgggtattt 180
tagcagcctg ggggcaggtt gtccctaattt ttctccaagt tcttcacatc agccagaatc 240
ccatctatgc ttgtctccag caaatggagg tggcccccctct gctgacgtgc cctctcttcc 300
agctctgaca tcatggcccg cagttggctg ttgatctggg tcttggctcg ggaaagctc 360
tgctccagta agaccagcccc ctcttcatct acactgagag gctggccat cagatgcagg 420
aggccgtcta atgtgttgag tgtgtcttgg attgttaaccc cagcgttctt ggctctggta 480
tcaaccttctt gggcttctgt aatcaccatc tgtactgcat ccatttcgt gtcgaactcc 540
agtccttcc t 551

<210> 249
<211> 181
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(181)
<223> n=A,T,C or G

<400> 249
atntccagag ggaccgttaag actggtaaca gtttacacca taagaggcga cgtggtcagc 60
cacaatgtct tcacacctcac aggggctcat cacggnggtc agggcaaggg ccccccagcat 120
cagagcttgc ttttaggatca tcctcttccc aaggcagcct tagcagttgc tgacctgccc 180
g 181

<210> 250
<211> 551
<212> DNA
<213> Homo sapiens

<400> 250
tctgttagcta ggatgagctg gctctcaaggc aaaagtttg cttccctgggt ccattttgtgg 60
tttacacttg ttattgaatg tacatcacaa attaaaagtct gcattttgtgg acgtaagaga 120
atgtgccgac tttggtaacc aggagatttc atgttactgg actgcctgtt gtcacgtatt 180
tctgttatgtt cacatccgca atgaaaaata ttaacctgaaat tttttcttag gagatcaacc 240
aaaataggag gtaatttttc tgcatccaaa tattcaagca actctccccc ttcataaggc 300
agtcaatgg tctcgaaatc tgatccgttt tttccccctga gcatcagaga atatccctca 360
tttccctgggtt atagattgac cactaaacat gacaaagtct cttgcataac aagtttctt 420
aacaagttca cattttcttta taatttctta acttcagggtt cttttccaca ttcttcaata 480
tacaagtcat aaagtttttg aaatacagat ttcttccac ttgataggttta 540
ggaggtctct 9 551

<210> 251
<211> 441
<212> DNA
<213> Homo sapiens

<400> 251
tgtctgtctt cccatccctgg ttacttatgag tcgctcttgg cagaaaggac cacagatgg 60
gagcttggca ctcgctccaa ctggccgaa aagaggacaa ccacccaaagt agtaggtaaa 120
aacacaattt tagcagcagt gaaataaaaaa gaggaaagtga ggtatggggcc aggccgcaac 180
tataattttttt ctgtctgtttt aggagaagct gaatccagaa gaaacacaag ctgtaaagt 240
agagaggaca gggagcaggg ccttggaga gcaggagagg acaggctgtc accaaggcgct 300
gtctggactc tgccctgaaa gatttgaattt ggacactgtc cagtcacgtg tgtggcaaac 360
cgtactccaa gcacttttttccac cacggcagag gaaggagctg ccatggctgt acccctgaac 420
gtttgtgggg ccagcgatgt 9 441

<210> 252
<211> 406
<212> DNA
<213> Homo sapiens

<400> 252
ttttttttt aacaagtaaaa aatttcttta tttgttgaca ataagataac ctacaggaa 60
aacacctgtatga aatcttattaa aaagttacta aaactaataa aagaatttag gaaggttata 120
gaatgtttaaaa ccaagacaca aaaatcaattt acattttctat ataatagcaa tgaacagata 180
ctgaaaattttt aaaaacttaaa tcattttaca aaagtatcac aatatgaaac actccgggat 240
aaattggata aaagatgtgc aagactgtac aaaagctaca aaacattttt gaaggaaattt 300
ggaagataga aacaagatag aaaatgaaaaa tattgtcaag agttttagat agaaaatgaa 360
aaacaagcta agacaagttt tggagaagttt tagaaagatag aaaaat 406

<210> 253
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (224)

<223> n=A,T,C or G

<400> 253

gaaggagttc agtagcaaag tcacacctgt ccaattccct gagcttgct cactcagcta 60
atgggatggc aaagggtggt gtgcattcat ctccaggcag aagcctctgc ccatccccct 120
caagggtctgc aggcccattt ctcattgtgc ctttgggtgg gcatctgtta acagaggaga 180
acgtctgggt ggcggcagca gctttgtct gagtgcctac aaanctaattt cttggtgct 240
gaaacatcat cattattaaa cttcagaaaa gcagcagcca tgttcagtc ggctcatgt 300
gcctcaactgc ttaagtgcct gcaggagccg cctgccaago tcccccttcc acacctggca 360
caactgggtc tgcacaaggc ttgtcaacc aaagacagct tccccctttt gattgcctgt 420
agactttgga gccaaagaaac actctgtgtg actctacaca caacttcaggt ggtttgtgct 480
tcaaagtcat tgatgcaact tgaaaggaaa cagtttaatg gtggaaatga actaccattt 540
ataa 544

<210> 254

<211> 339

<212> DNA

<213> Homo sapiens

<400> 254

tggcatttcg ggcagtgtct tctgcatttc ctaggaacctt cgggagccgc agctccggcg 60
cctggtagcg agaggccgggt tccggagatc cccgcctcac ttctgtccac tgggtttagg 120
ggtagtgcctt gcaaattgtt agtgatttgc tcaaggtgcc catttcgcag gaattggagc 180
ccaggccagt tctctgagcc tatcatttgg gctaaaggag tgcgtatca gaatgggtgtc 240
tggacggttc tacttgtctt gcctgtgtctt ggggtccctg ggctctatgt gcattctt 300
caactatctac tggatgcagt actggcgtgg tggctttgc 339

<210> 255

<211> 405

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(405)

<223> n=A,T,C or G

<400> 255

gagttttttt tttttttttt caattaaana tttgatttat tcaagtatgt 60
gaaaacattn tacaatggaa actttttta aatgctgtcat gtntctgtct atggaccacn 120
cacatacagc catgtgtttt caaaaaactt gaaatgccat tgatagtta aaaactntac 180
ncccgatgga aaatcgagga aaacaattta atgtttcatn tgaatccana ggngcatcaa 240
attaaatgac agtccactt ggcaaaataat agtctttact tgatggatc caaaaaaaaaa 300
tgggtgggaa tggataaaattt caaaaatgtc tccccaaagg ngggngggtt taaaaaagt 360
tcaggncaca acccttgcan aaaacactga tgcccaacac antga 405

<210> 256

<211> 209

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (6)

<223> n=A,T,C or G

<400> 256
gggcangtct ggtcctctcc ccacatgtca cactctcctc agcctctccc ccaaccctgc 60
tctccctctt cccctgcctt agcccgaggaa cagagtctag gaggagcctg gggcagagct 120
ggagggcagga agagagcact ggacagacag ctatggttt gattgggaa gaggttagga 180
agttagttct taaagacctt ttttttagta 209

<210> 257
<211> 343
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(343)
<223> n=A,T,C or G

<400> 257
tctggacacc ataatccctt ttaagtggct ggatggtcac accrctccca ttgacaagct 60
gggttaagtc aataagggtga ctaggatcaa cacgacccaa atcaataaga tactgcagtc 120
tattgagact caaaggctta tactggcgctc tgaaactatgt tccttcgtta aacccgtatt 180
ttggggattcg gatgtaaaat ggagtcgtgc ctccctcaaa gcccaagcgg ggccgggttc 240
ctctttgcct ttctccttta tggcctctgc cacatttct acctttctc cgacctcttg 300
gtcttnctc nggtttcttg gagccggat tcggctttaa gtn 343

<210> 258
<211> 519
<212> DNA
<213> Homo sapiens

<400> 258
gcggcttctg acttctagaa gactaaggct ggtctgtgtt tgcttgttg cccacctttg 60
gctgataccc agagaacctg ggcacttgct gcctgatgcc caccctgcc agtcattctt 120
ccattcaccc agcgggaggt gggatgtgag acagcccaca ttggaaaatc cagaaaaccg 180
ggaacaggaa ttggcccttc acaattctac tccccagatc ctctccctg gacacaggag 240
acccacaggc caggacccta agatctgggg aaaggaggctc ctgagaacct tgaggtaccc 300
tttagatcctt ttctaccac tttccatgg aggattccaa gtcaccactt ctctcaccgg 360
cttctaccag ggtccagac taaggcgttt tctccatagc ctcaacattt tggaatctt 420
cccttaatca cccttgctcc tcctgggtgc ctggaaagatg gactggcaga gacctcttg 480
ttgcgttttg tgctttgtatc ccagaatgc cgccttagtt 519

<210> 259
<211> 371
<212> DNA
<213> Homo sapiens

<400> 259
attgtcaact atatacacag tagtgaggaa taaaatgcac aaaaaacaat ggatagaata 60
tggaaaatgtc ttctaaatat gaccagtcta gcatagaacc ttctttctt ccttctcagg 120
tcttccagct ccatgtcattc taacccactt aacaaacgtg gacgtatcgc ttccagaggc 180
cgtcttaaca actccatttc caaaagtcat ctccagaaga catgtatccc ctatgatttc 240
ttttaaacaa atgagaattt acaagatgtg taactttcta actctatccc atcatacgtc 300
ggcaacctct ttccatctag aagggttaga tgtgacaaat gttttctatt aaaagggttgg 360
ggtggagttg a 371

<210> 260
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(430)
<223> n=A,T,C or G

<400> 260
ttggatttt tgacttgcga tttcagttt tttactttt tttttttttt ttttganaaaa 60
tactatattt attgtcaaaag agtggatcat aggtgagtgt tcacatctccc tctccatgccg 120
gtatactctg ctccgctgtt tcagtaaaag ttttccgtag ttctgaacgt cccttgcacca 180
caccataana caagcgcaag tcactcanaa ttgccactgg aaaactggct caactatcat 240
ttgaggaaag actganaaaag cctatcccaa agtaatggac atgcaccaac atcgcggtac 300
ctacatgttc ccgtttttct gccaatctac ctgtgtttcc aagataaatt accacccagg 360
gagtcacttc ctgctatgtg aacaaaaacc cggtttctt ctggaggtgc ttgactactc 420
tctcgngagc 430

<210> 261
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (178)
<223> n=A,T,C or G

<400> 261
tcctgacgat agccatggct gtaccactta actatgattc tattccaact gttcagaatc 60
atatcacaaa atgacttgta cacagtagtt tacaacgact cccaaagagag gaaaaaaaaa 120
aaaaaaaaagacg cctcaaaatt cactcaacctt ttgagacagc aatggcaata ggcagcanag 180
aagctatgct gcaactgagg gcacatatca ttgaagatgt cacaggagtt taagagacag 240
gctggaaaaaa atctcataact aagcaaacag tagtatctca taccaagcaa aaccaagttag 300
tatctgctca gcctgccgt aacagatctc acaatccacca actgtgtttt aggactgtca 360
ccaaa 365

<210> 262
<211> 500
<212> DNA
<213> Homo sapiens

<400> 262
cctagatgtc atttgggacc cttcacaacc attttgaagc cctgttttag tccctggat 60
atgtgagctg ttcttatgca taatggat tccgggttaa caacagtccc ctgttgtggct 120
tctattctga atccctttct ttcaccatgg ggtgcctgaa gggtgtgtga tgcataatgg 180
acaatggcac ccagtgtaaa gcagctacaa ttaggagtgg atgtgttctg tagcatccta 240
tttaaataag cctattttat cctttggccc gtcaactctg ttatctgctg cttgtactgg 300
tgcctgtact ttctgactc tcattgacca tattccacga ccatgggtgt catccattac 360
ttgatcctac ttacatgtc tagtctgtgt gggtgggtgt gaataggtt ctttttacat 420
ggtgctgcca gcccagctaa ttaatggtgc acgtggactt ttagcaagcg ggctcaactgg 480
aagagactga acctggcatg 500

<210> 263
<211> 413
<212> DNA
<213> Homo sapiens

<400> 263
ctcagagagg ttgaaagatt tgcctaccaa agggacagt atgaagctaa gctctagatc 60
caggatgtct gacttcaaat tgaaactccc aaagtaatga gtttggaaagg gtgggggtgtg 120
gcctttccag gatgggggtc ttttctgctc ccagcgatata gtggaaacccc tgctgcacc 180
tggttggcg tggtgcttc ccaaagggtt ttttttagg tccgtcgctg tcttgtggat 240
taggcattat tatctttact ttgtctccaa ataacctgga gaatggagag agtagtgacc 300
agctcaggc cacagtgcga tgaggaccat ctctcacct ctctaaatgc aggaagaaac 360
gcagagtaac gtggaaagtgg tccacaccta ccgccagcac attgtgaatg aca 420

<210> 264
<211> 524
<212> DNA
<213> Homo sapiens

<400> 264
tccaatgggg ccctgagagc tgtgacagga actcacactc tggcactggc agcaaaaacac 60
cattccaccc cactcatcg tctgtgcaccc atgttcaaac tttctccaca gttccccat 120
gaagaagact catttcataa gtttggct cctgaagaag tcctgcacc cacagaaggg 180
gacattctgg agaaggctcg cgtgcattgc cctgtgtttt actacgttcc cccagagctc 240
attaccctct ttatctccaa cattgggtggg aatgcacccctt cctacatcta ccgcctgtatg 300
agtgaactct accatcctga tgatcatgtt ttatgaccga ccacacgtgt cctaagcaga 360
ttgcttaggc agatacagaa tgaagaggag acttgagtgt tgctgtgaa gcacatcctt 420
gcaatgtggg agtgcacagg agtccaccta aaaaaaaaaaa tccttgatac tggtgcctgc 480
cttttagtc accccgtAAC aaggcacaac atccaggact gtgt 524

<210> 265
<211> 344
<212> DNA
<213> Homo sapiens

<400> 265
tcctttcttc tacttcagga gatgattcaa agttacttgtt ggacatttct ttaagttctg 60
aagacaaatg agacaggatt tggctgcgg gttcttcaga cttctctacc acctccatta 120
actcttcatc ttggcttgc acgttcaatg cactatTTT ctctttgtt tctggagatg 180
accaggcacc acttcttctt cttggcgggg ttcttaagtgt gtctttgaat accagtgaag 240
actcaggcct atcctgtact ggaaggac taaatttgc tttctgtcta ggaggtgtatg 300
cagtagcatc ctccgtggg ggttaaggcca ttttctcttt ttGA 344

<210> 266
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (78)
<223> n=A,T,C or G

<400> 266
ccacaatgtc cataacttga gcaggcttg gcatcccacc acccccttca gaccaataca 60

cactatgttg gaggaacnac tttaaaatgt aaaatgagaa atgggcactg aacactccat 120
cctcaactccc aacagcccc acacacacct cttcaactgc tatccaaaca tggaggagct 180
cttgtgaaag agaggctcaa caccaataa 210

<210> 267
<211> 238
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(238)

<400> 267
tcggncctcc caccctctna ctgaaattct ntgaaattct cccctttggg atgaggatgg 60
caaaaaaagg catgtacccct cccaacctgg gacccgaccc aataccctaa catcctgctg 120
acagtggctg ttctcgctgg gcaggcgtcc caaaggcacat cgagccagat tcagggcagag 180
tggaaactggc ccctcagcca tcagtggagg tggcctggga ggctctaccc tgaacggg 240

<210> 268
<211> 461
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (459)
<223> n=A,T,C or G

<400> 268
tcctcaagga catgccccctt gatagaaaact cagttcctgt ctccagttcc ctccctggacc 60
tgatccccca aatgcaggc ctggactat atccagttcc ttatttcag aggcccatgc 120
acaagatgca cagcaaataa gtgctgaata aagacccagc tactgttagc ttacccctgct 180
ccaaacatcc accaagtccct cagcaaagag ggcacatccat tcaccccttc taaaaacaca 240
ctgagctccc cagtctatac cccaaagatat gcttggctcc caactatccc tcctctctca 300
tctccaagcc agtttccctt ttcttaagtat actgatattt ccaaagacac tgacaatctt 360
ctttccctac ctctcccaag tgacttagtt tgcagcagga gctctataag tccttagtata 420
cagcagaagc tccataaatg tgtgctgacc taacattang c 461

<210> 269
<211> 434
<212> DNA
<213> Homo sapiens

<400> 269
ctgtgttgtt gagcaccgat tcccactcaa tatggcgtgg cttacagtct tcatttagtt 60
cccgctccca accagaatga ggaatgatca cttcatctgt caaggcatgc agtgcattgt 120
ccacaatctc cattttgatt gagtcatggg atgaaagatt ccacagggtt ccggtataaa 180
cttcagtaag gtccatatca cgaggcttcc gaagcaatcg cacaaggcga ggcacaccat 240
cacagttttt tatggcaatc ttgttatccct ggtcacgtcc aaaagagata ttcttgagag 300
ctccacaggc tccaagggtgc acttcccttt tgggatggtc taacaatccc accagtactg 360
ggatgccctt gagcttccgc acgtcagtttc tcacccgttc attgcggtag cataagtgtt 420
gcaggtatgc aaga 434

<210> 270

<211> 156
<212> DNA
<213> Homo sapiens

<400> 270
ctgcaccaggc gattaccagt ggcattcaaa tactgtgtga ctaaggattt tgtatgctcc 60
ccagtagaac cagaatcaga caggtatgag ctatcaaca gcaagtcttt gttggattcg 120
atggtagctca ggatctgctg aaggtcgagg gagtt 156

<210> 271
<211> 533
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(533)
<223> n=A,T,C or G

<400> 271
ccactgtcac ggtctgtctg acacttaactg ccaaacgcac ggcaaggaaaa aactgcttag 60
tgaagaacctt agaagctgtg gagacaccttgg ggtccacgtt caccatctgc tctgataaaaa 120
ctggaactct gactcanaac cggatgacag tggcccacat gtggtttgac aatcaaatcc 180
atgaagctga tacgacagag aatcagagtg gtgtctcttt tgacaagact tcagctaccc 240
ggcttgcctt gtccagaatt gcaggctttt gtaacaggggc agtgtttcag gctaaccagg 300
aaaacctacc tattcttaag cgggcagttg caggagatgc ctctgagtc gcactcttaa 360
agtgcataga gctgtgttgtt ggntncgtga aggagatgag agaaagatac nccaaaatcg 420
tcgagatacc cttcaactcc accaacaagt accagttgtc tattcataag aaccccaaca 480
catcgagcc ccaacacctg ttgggtgatga agggcgcccc agaaaggatc cta 540

<210> 272
<211> 630
<212> DNA
<213> Homo sapiens

<400> 272
tggatttttt ctttttcttt tggatgtttt atactttttt ttcttttttcttcttatttc 60
ttttcttcgc cttcccgatc ttctgtcttc cagttttccat cttcaaaactt ctatcttc 120
caaattgttt catccatcca ctcccaatta atctttccat tttcgctctgc gtttagaaaa 180
tgcgttaact aggctttaaa tgacgcaatt ctccctgcgt catggatttc aaggtctttt 240
aatcaccttc ggtttaatct ctttttaaaa gatcgcccttc aaattttttt aatcacctac 300
aacttttaaa ctaaacttta agctgtttaa gtcacccatca ttttaatcta aaagcattgc 360
cctctattt gatattaaatc ggggctctgt agtcttttctt ctcaattttc ttttaataac 420
atttttact ccatgaagaa gcttcatctc aacccctccgtc atgtttttaga aaccttttat 480
ctttcccttc ctcatgctac tcttcttaagt cttcatattt tctcttaaaa tcttaagcta 540
ttaaaattac gttaaaaact taacgctaag caatatctta gtaacccattt gactatattt 600
tttaagtatgt tttttttttt 630

<210> 273
<211> 400
<212> DNA
<213> Homo sapiens

<400> 273
tctggtttgc cttcccgatc attctgaatc tagacttgct cagccataatc aagttccgtt 60

acaaccagaa gcgcacacagg ttcctttgggt atcatccaca agtgagggggt acacagcata 120
 tcaacccttg taccagcctt ctcatgtcac agagcaacga ccacagaagg aaccaattga 180
 tcagatttcg gcaacaatct cttaaatac agaccagact acagcatcat catcccttcc 240
 tgctgcgtct cagcctcaag tatttcaggc tgggacaaggc aaacctttac atagcagtgg 300
 aatcaatgtt aatgcagctc cattccaatc catgcaaacg gtgttcaata tgaatgcggcc 360
 agttccctcct gttaatgaac cagaaaacttt aaaacagcaa 400

<210> 274
 <211> 351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (2)
 <223> n=A,T,C or G

<400> 274
 tntgagtatg tcccagagaa ggtgaagaaa gcggaaaaaga aattagaaga gaatccatat 60
 gaccttgatg cttggagcat ttcattcga gaggcacaga atcaacctat agacaaaagca 120
 cggaaagactt atgaacgcct tggcccccag ttccccagtt ctggcagatt ctggaaactg 180
 tacattgaag cagaggttac tatttttattt tatattttct tatatcagta ttgcagatt 240
 cactgttagt atagaaaaca agtttaggaac atagccaatt aggacaagga ggattttaaat 300
 gtgtcttacc tttattttgtt aaaaataggtt taaaggagttt attaaaaatgtt a 360

<210> 275
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(381)
 <223> n=A,T,C or G

<400> 275
 gcgnggtcg nnnccagggtc tgagaagccc ataccactat ttgttgagaa atgtgtggaa 60
 tttattgttggat ataccagggtt atgtaccgaa ggactctacc gtgtcagcgg gaataaaact 120
 gaccaagaca atatcaaaa gcagtttgcattt caagatcata atatcaatct agtgtcaatg 180
 gaagtaacag taaatgttgtt agctggagcc cttaaagctt tctttgcaga tctgccat 240
 cctttatccatattcttct tcattccagaa ctatttgcaga cagcaaaaat cccggataaaa 300
 acagaacgtc ttcatgcctt gaaagaaaattt gttaagaaaat ttcatccctgtt aaactatgtt 360
 gtatttcgat acgtgataac a 381

<210> 276
 <211> 390
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (5)
 <223> n=A,T,C or G

<400> 276

gctcngactc cggcgggacc tgctcgagg aatggcgccg ccgggttcaa gcactgtctt 60
cctgttggcc ctgacaatca tagccagcac ctgggcctcg acgcccactc actacctcac 120
caagcatgac gtggagagac taaaagcctc gctggatcgc ctttcacaa atttgaatc 180
tgccttctac tccatcgtag gactcagcac cttgggtgtc caggtgccag atgcaaagaa 240
agcatgttacc tacatcgat ctaaccttga tcccagcaat gtggattccc tcttctacgc 300
tgcccaggcc agccaggccc tctcaggatg tgagatctt atttcaaatg agaccaaaga 360
tctgcttctg gcagacctcg gccgcgacca 390

<210> 277

<211> 378

<212> DNA

<213> Homo sapiens

<400> 277

tgggaacttc tgggttagga cgttgtctgc tatctccagt tccacagacc caaccagttt 60
cgatggttt ggaccattta tgccggatt cgacatcatt ccctataatg atctgcccgc 120
actggagcgt gcttctcagg atccaaatgt ggctgcgtc atggtagaac caattcaggg 180
tgaagcaggc gttgttggtc cggatccagg ttacctaatg ggagtgcgag agctctgcac 240
caggcaccag gttctctta ttgctgatga aatacagaca ggattggcca gaactggtag 300
atggctggct gttgattatg aaaatgtcag acctgtatata gtcctcttg gaaaggccct 360
ttctggggc ttatacc 378

<210> 278

<211> 366

<212> DNA

<213> Homo sapiens

<400> 278

ggagggcaca ttctttca cctcagagtc ggtcgaaaaa ggccacccag ataagattt 60
tgaccaaacc agtgtatgtc tccttgatgc ccacccatcg caggatctg atgccaaagt 120
agcttgtgaa actgttgcta aaacttggat gatccctt gctggggaaa ttacatccag 180
agctgtgtt gactaccaga aagtggttcg tgaagctgtt aaacacattt gatatgtga 240
ttctccaaa ggttttact acaagacttg taacgtgtc gtagccttgg agcaacagtc 300
accagatatt gctcaagggtg ttcatcttga cagaaatgaa gaagacattt gtgctggaga 360
ccaggg 366

<210> 279

<211> 435

<212> DNA

<213> Homo sapiens

<400> 279

cctaagaact gagacttgcg acacaaggcc aacgacctaa gattagccca gggtttagc 60
tggaaagacct acaacccaaag gatgaaaggc ccctgtcaca aagcctaccc agatggatag 120
aggacccaaag cggaaaaagat atctcaagac taacggccgg aatctggagg cccatgaccc 180
agaacccagg aaggatagaa gcttgaagac ctggggaaaat cccaaatgaa gaaccctaaa 240
ccctacccct tttcttattgt ttacacttct tactctttaga tattttccagt tctcctgttt 300
atctttaagc ctgattctt tgagatgtac tttttgtatgt tgccggttac cttagattt 360
acaagtatta tgccctggcca gtcttgagcc agctttaaat cacagctttt acctattttgt 420
taggctatag tgttt 435

<210> 280

<211> 435

<212> DNA

<213> Homo sapiens

<400> 280
tctggatgag ctgctaactg agcacaggat gacctggac ccagcccgac caccggaga 60
cctgactgag gccttcctgg caaagaagga gaagggcaag gggagccctg agagcagtt 120
caatgatgag aacctgcgca tagtggtggg taacctgttc cttgccggg tggtgaccac 180
ctcgaccacg ctggcctggg gcctcctgtc catgatccta cacctggatg tgcagcgtga 240
gcccagacct gtccggcgg ccgctcgaa ttccagcaca ctggcggccg ttactagtgg 300
atccgagctc ggtaccaagc ttggcgtaat catggtcata gctgtttcct gtgtgaaatt 360
gttatccgct cacaattcca cacaacatac gagccggaag cataaagtgt aaagcctggg 420
gtgcctaattg agtga 435

<210> 281
<211> 440
<212> DNA
<213> Homo sapiens

<400> 281
catctgatct ataaatgcgg tggcatcgac aaaagaacca ttgaaaaatt tgagaaggag 60
gctgctgaga tggaaaaggc ctccttcaag tatgcttggg tcttggataa actgaaagct 120
gagcgtgaac gtggtatcac cattgatattc tccttgcgg aatttgagac cagcaagttac 180
tatgtgacta tcattgtatgc cccaggacac agagacttta tcaaaaaacat gattacagg 240
acatctcagg ctgactgtgc tgccttgatt gttgctgctg gtgtggta atttgaagct 300
ggtatctcca agaatggcga gacccgagag catgcccttc tgcttacac actgggtgtg 360
aaacaactaa ttgtcggtgt taacaaaaatg gattccactg agccccctac agccagaaga 420
gatatgagga aatttgttaag 440

<210> 282
<211> 502
<212> DNA
<213> Homo sapiens

<400> 282
tctgtggcgc aggagccccc tccccccggca gctctgacgt ctccacggca gggactggtg 60
cttcctcgag ctccactcc ttagactccg gtggaaagtga cgtggacctg gateccactg 120
atggcaagct cttcccccagc gatggtttc gtgactgcaa gaagggggat cccaaagcacg 180
ggaagcggaa acggggccgg ccccgaaagc tgagcaaaaga gtactggac tgtctcgagg 240
gcaagaagag caagcacgca cccagaggca cccacctgtg ggagttcatc cgggacatcc 300
tcatccaccc ggagtcacac gagggcctca tgaagtggga gaatcggcat gaaggcgtct 360
tcaagttctt gcgctcccgag gctgtggccc aactatgggg caaaaagaaaa aagaacagca 420
acatgaccta cgagaagctg agccgggcca tgaggtacta ctacaaaacgg gagatcctgg 480
aacgggtgga tggccggcga ct 502

<210> 283
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(433)
<223> n=A,T,C or G

<400> 283
ccatattaga ttactggaac atctaaggcat cagtgtgtga ccatgcgaac aaaagacttc 60
ggggagtgta tattttaaa aaggttatg tgcgtcgagg cagttgtaaa agatttactg 120

cagaatcaan cccacttta ggcttangac caggttctaa ctatctaaaa atattgactg 180
 ataacaaaaa gtgttctaaa tgtggctatt ctgatccata nttgnntttt aaagaaaaaa 240
 antgtntata cagaaagagt ntaaaagttc tgtgaattna atgcaattt gnncnccantc 300
 ttgacttccc aaanacttga ttnataccct tnactcctnt cnnttcctgn ntttcnttaa 360
 nntcaatnat tnggnagtnn anggcncntn gnanaaacacc nttncncntc ccncgcaatc 420
 canccgcctt nan 433

<210> 284
<211> 479
<212> DNA
<213> Homo sapiens

<400> 284
tctggaagga tcaggatct gagcaaagcc aagtttactt aagctaagcc acttggctt 60
gggtcaagca gtttggtttc taataagcat cattcctgat cattagagca aagggtatgaa 120
tgctcctctt ggaatgatac agggatctg ccactgggag agtgttgctc agtgttagag 180
tagcagcaat gacagaatga cagcgactt ctgagtcac ccagtacttt tagtaccccg 240
tcactatgtg aataaaggca gctagaaaaat ggactcaatt ctgcaagcct tcattggcaac 300
agcccatatt aagacttcta gaacaagttt aaaaaaaaaatc ttccatttcc atccatgcat 360
ggaaaaagggg cttagtata gtttagatg gatgtgtgtta taataataaa atgataagat 420
atgcatagtg gggaaataaa gcctcagagt cttccagta tggggaatcc attgttatct 480

<210> 285
<211> 435
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(435)
<223> n=A,T,C or G

<400> 285
tttttttttt tttttttttt tcaatanaaa tgccataatt tattccattt tataaaaaaag 60
tcatccttat gtaacaaaat gtnttcttan aanaanaaat atattatttc aggtcataaaa 120
taatcagcaa acatacaact gttggcaact aaaaaaaaaac ccaacactgg tattttccat 180
cagngctgaa aacaacactg cttaaanata tatttacagg gatagtncag tnctaaaaa 240
caaaaattga ggtattttgg ttcttcttagg agtagacaat gacattttgg gangggcaga 300
ccccctnnccc aaaaaataaa ataagggnat nttcttcant atngaannnn gggggcgccc 360
cggggaaaan naaaccttgg gnnggggtt tggcccaagc ctttggaaaaaa aaantttntt 420
tcccaaaaaaa aacng 435

<210> 286
<211> 301
<212> DNA
<213> Homo sapiens

<400> 286
cctggtttct ggtggccctt atgaatccca tggtaggggtgc agaccgtact ccatccctcc 60
ctgtgagcac cacgtcaacg gctccggcc cccatgcacg ggggagggag ataccccaa 120
gtgttagcaag atctgtgagc ctggctacag cccgacctac aaacaggaca agcactacgg 180
atacaattcc tacagcgctt ccaatagcga gaaggacatc atggccgaga tctacaaaaa 240
cggccccgtg gagggagctt tctctgtgtt ttcggacttc ctgctctaca agtcaggagt 300
g 301

<210> 287
<211> 432
<212> DNA
<213> Homo sapiens

<400> 287
tccagttgt tgccagcatg agaacggcca ttgatgacat tgaacgcgg gactggcagg 60
atgacttcag agttgccagc caagtcagcg atgtggcggt acagggggac ccccttctca 120
acggcaccag ctttgagac ggcaagggac acccccagaa tggcggtcgc accaaactta 180
gatttatttt ctgttccatc catctcgatc atcagttgtt caatcttctc ttgttctgtg 240
acgttcagtt tcttgctaac cagggcaggc gcaatagttt tattgatgtg ctcAACAGCC 300
tttgagacac ccttccccat atagcgatgc ttatcattgtt cccggagctc tagggcctca 360
tagataccag ttgaaggcacc actgggcaca gcagctctga agagaccttt tgaggtgaag 420
agatcaacctt ca 432

<210> 288
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (254)
<223> n=A,T,C or G

<400> 288
tctggctcaa gtcaaagtcc tggcctctt ctccgcctcc ttcttcatca tagtaataaa 60
cgttgtcccg ggtgtcatcc tctggggca gtaaggcgc tttgaccacc gctctccctcc 120
gaagaaacag caagagcagc agaatcagaa ttagcaaagc aagaattcctt ccaagaatcc 180
ccagaatggc aggaatttgc aatccgtctt cgacaggctg tgccttccta cagacgcggg 240
cgcccccttc acantcacac acgctgaccc ttaagggtt cacttggctt ttattctgtt 300
tatccatgag cttgagattt atttt 326

<210> 289
<211> 451
<212> DNA
<213> Homo sapiens

<400> 289
gtccccgggt ggctgtgccg ttggcctgt gcggtcactt agccaagatg cctgaggaaa 60
cccagaccca agaccaacccg atggaggagg aggaggttga gacgttcgc tttcaggcag 120
aaattggcca gttgtatgtca ttgatcatca atactttctt ctcgaacaaa gagatcttc 180
tgagagagct catttcaaat tcatacgatg cattggacaa aatccggat gaaagcttga 240
cagatcccgag taaatttagac tctggaaag agctgcataat taaccttata ccgaacaaac 300
aagatcgaac tctcactatt gtggatactg gaatttggaaat gaccaaggct gacttgcata 360
ataaccttgg tactatcgcc aagtctggaa ccaaagcgat catggaaatgctt tgccaggctg 420
gtcagatata ctctatgatt ggaccccgcc 451

<210> 290
<211> 494
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (421)

<223> n=A,T,C or G

<400> 290

ttttttttt tcaaaaacagt atatttatt ttacaatagc aaccaactcc ccagtttgg 60
 tcaattgtga catctagatg gcttaagatt actttctggg ggtcacccat gctgaacaat 120
 attttcaat cttccaaaca gcaaagactc aaaagagatt ctgcatttca catcagttca 180
 caagttcaag agtcttccat ttatcttagc ttttggaaa aattatctt gaggtagaag 240
 gacaatgacg aagccactta attccttggc tctgcataaa agcagattt ttcatacaca 300
 cttcatttat gtgaataaaag cagatgatga taaaatgttc tcttattttt gtttaatcag 360
 tagtgttagt gatgccagaa acttgtaaat gcacttcaaa ccaattgtgg ctcaagtgt 420
 ngtggttccc caaggcttgtt accaatgaga ctggggtttg ggaatttagtt ggtcatcata 480
 cctcctgctg ccca 494

<210> 291

<211> 535

<212> DNA

<213> Homo sapiens

<400> 291

tgcgtgtctt aacatgaaaa caaactttgt gctgtttggg tcattgtatg cattgtatgg 60
 gtccttgcctc tcatcatggg gtgtctgacc atccaaacctg cagtaactcat aatttctcca 120
 catgcaataa tcttccaaaa tgtccaaatac ctttgcatt tgactgaaga ttagtactcg 180
 tgaacccctgt tcttttaact tagggaggcag cttgtctaaa accaccatgg tgccactgtt 240
 ggttactaga tgcataatctg ttgtataagg tggaccagggt tctgctccat caaagagata 300
 tggatgatca caacattttc tcaactgcat taggatgttc aataacccca ttttgcctcat 360
 cttgcctgtctt gagttgatca tatctatatac cttcattaaat atccgagttt accatcccc 420
 ttgcattttt ctgaggccca catagattt tacttccttc tttggaggca aactcttttc 480
 aacatcagcc ttaattcgac gaaggaggaa tggacgcaaa accatatgaa gcctc 540

<210> 292

<211> 376

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(376)

<223> n=A,T,C or G

<400> 292

tacnagcccg tgctgatcga gatccctgggt gagggtatgg atccttcctt cgtgtgctt 60
 aaaattggag cctgccccctc ggcccataag cccttgggg gaactgagaa gtgtatatgg 120
 ggcccaagct actgggtccca gaacacagag acagcagccc agtgcaatgc tgtcgagcat 180
 tgcaaacgcc atgtgtggaa ctaggaggag gaatattcca tcttggcaga aaccacagca 240
 ttggttttt tctacttggc tgcgtgggg aatgaacgca cagatctgtt tgactttgtt 300
 ataaaaatag ggctccccca cctcccccat ttttggcatttgcatttgnag cattgtgtc 360
 tgcaagggag ccccta 376

<210> 293

<211> 320

<212> DNA

<213> Homo sapiens

<400> 293

tcggctgctt cctggctcgg cggggatggg tttgctttgg aaatccctcta ggaggctcct 60
 cctcgcatgg cctgcagtc ggcagcagcc ccgagttgtt tcctcgctga tcgatttctt 120
 tcctccaggt agagttttct ttgcttatgt tgaattccat tgcctctttt ctcacacag 180
 aagtgtatgtt ggaatcggtt cttttgttttgc tctgatttat ggttttttta agtataaaaca 240
 aaagttttttt attagcattc tgaaagaagg aaagtaaaat gtacaagttt aataaaaagg 300
 ggccttcccc tttagaata 320

<210> 294
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 294
 ctgtcataaa ctggctcggg gtttctgacg actccttgtt caccaaatgc accatttcct 60
 gagacttgcg ggcctctccg ttgagtcac ttggctttct gtcctccaca gctccattgc 120
 cactgttgcg cactagctt ttcttctgccc cacacccctt tcgactgttg actgcaatgc 180
 aaactgcaag aatcaaagcc aaggccaaga gggatgccaa gatgatcagc cattctggaa 240
 tttggggtgtt ccttatacgaa ccagagggtt tgtttgcctt accttcttgc ctcccatgtg 300
 agtgtccatc tgattcagat ccatgagttt tatgggaccgc cccactgggg tggaatgtg 360

<210> 295
 <211> 584
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (558)
 <223> n=A,T,C or G

<400> 295
 cctgagttgg gctgactgcc agagacagac ccctctgggt ctgggtgaac cagccaggca 60
 tttacctcag tgggtggcac ctggAACCTG tccaggGCC tcacctgact gaggagCCGC 120
 cggcagtga agtaattgtc caggtctatg ctcttgggtt ggataccata gccatccaag 180
 gtattcctca gggtgtggaa ctgggtctga gtataggcag aactggggcc caggatgatc 240
 tccccggatgtt ggggaagctg tgagggtcagg taagtatcca cgtccaccccg taccggaaatc 300
 aaactcagca gaatgggtgaa ctggagaagt cttccgttta agtatttctt cagagaaagc 360
 attgctgaag gaccagaatg tttatgtttt ttgggtttta aaatcttcca aaagacaaaat 420
 caaggccact gctctgccgc tccagccagc aggttaccct cctcagtgatc aaaccccgta 480
 cccacccctg gcagaacaca agggatgagc tccctgacgg ccccagagga aagcacaccc 540
 tgtggagcca agggcaanga cacactccag accacattca ct 584

<210> 296
 <211> 287
 <212> DNA
 <213> Homo sapiens

<400> 296
 ccttatcatt cattcttagc tcttaattgt tcattttgag ctgaaatgct gcattttat 60
 tttaacccaaa acatgtctcc tattctgggtt ttgttagcct tcctccacat cttttctaaa 120
 caagattttt aagacatgtt ggtgtttgtt catctgttaac tctaaaaagat cttttttaaa 180
 ttcaagtccatc agaaagaggg gttgtgtcc cttcaagagtg tttaatggca aggccagccct 240
 gtctgaagga cacttccatc ctaagggaga gtggatatttgc cagacta 287

<210> 297

<211> 457
<212> DNA
<213> Homo sapiens

<400> 297
ccaattgaaa caaacaggc ttccaccac tgattaagag tgggggtggca 60
ggtatttaggg ataatatattca tttagccttc tgagctttct gggcagactt ggtgacctt 120
ccagctcccg cagccttctt gtccactgct ttgatgacac ccacgcac tgcgtctc 180
atatcacgaa cagcaaagcg acccaaagggt ggatagtctg agaagctctc aacacacatg 240
ggcttgcagg gaaccatatac aacaatggca gcatcaccag acttcaagaa tttagggcca 300
tcttcagct ttttaccaga acggcgatca atctttctt tcagctcagc aaacttgcatt 360
gcaatgttag cctgttgcca atccaatacata ggggcatacg cggcgcttat ttggcctgga 420
tggttcagga taatcacctg agcagtgaag ccagacc 457

<210> 298
<211> 469
<212> DNA
<213> Homo sapiens

<400> 298
tctttgactt tccttgcata cctcctctgg agatctcaaa ttctccagggt tccatgtctcc 60
cagagatctc aatgatttctt gattttctc ttccaggagt ctgaatgtct ctgggttac 120
ttccacacagac tccagtgggtt cttgaatttc cttttctaga ggatttatttgc cccctgtatt 180
tattttcttctt ggagtccaca gtgggtgtt agtttctggta gatttctgtt ttccagggtt 240
ctcttgcctcc gcagacttca gtgattcttagt gatctctgtt tctaaagatt ttactgcctc 300
tatgtctctt tctttgatgtt actttaagaa ctcttgattt tcattttcaa gaggtcttagc 360
tatctcttgg tcaagagact tcagtggttc tagatccact ttttctgggg gtcttaatgt 420
catctgatcc tggttccctca gggccctccg tggctgttga gtctttttt 469

<210> 299
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(165)
<223> n=A,T,C or G

<400> 299
tctgtggaga ggatgagggtt gagggagggtg gggtatntcg ctgtctgac cttaggtaga 60
gtcctccaca gaagcatcaa antggactgg cacatatggta ctcccttac aggccacaat 120
gatgtgtctc tccttcgggc tggncggta tgcacagttt gggta 165

<210> 300
<211> 506
<212> DNA
<213> Homo sapiens

<400> 300
tctgaggaaa gtttgggtt attagtattt gctccaggcga acctccaagt tttctccatt 60
gcggacaacg taactaccag ctccctggct cagtggttcg cttccactca gaagtccccca 120
gtagggtctg tcattattgt tggcacatag gcccgttgcata caggtgtat agggccccca 180
tgagcgctcc tccattgtga aaccaaataat agtacatttc atttctggg ctccatccat 240
cacactgagg aagacagaac catttagcactt agtgcatttgcgttgcattatgtt 300

tctcacagag taattgacgg agatatatga ttgtgagtca ggagggtgtca cagttataagg 360
ctcatcagcg gagatgtga agttaacctga agcagagacg caagaagagt ctttgttaat 420
atccaagaag gtcttccca tcagggcagg taagacctgg gctgcagcgt tggattgct 480
gaatgctcct tgagaaattt ccgtga 506

<210> 301
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(304)
<223> n=A,T,C or G

<400> 301
tcctaaggca gagccccat cacccaggc ttctcagttc ccttagccgt cttaactcaac 60
tgcccccttc ctctccctca gaatttgtt ttgctgcctc tatcttgtt tttgtttttt 120
cttctggggg gggcttagaa cagtcctgg cacatagtag gcgctcaata aatacttgtt 180
tggtaatgt ctccctctc tttccactct gggaaaccta ngntctgcc attctgggtg 240
accctgtatt tntttcttgtt gccattcca tttgnccagn taatacttcc tctaaaaat 300
ctcc 304

<210> 302
<211> 492
<212> DNA
<213> Homo sapiens

<400> 302
ttttcagtaa gcaactttc catgctctta atgtattcct ttttagtagg aatccygaag 60
tattagattt aatggaaaag cactgccc ctctgtctag gggtcacaaa ttgaaatggc 120
tcctgtatca catacgagg tcttgttat ctgtggcaac agggagttc ctattact 180
cttatttgc tgctgtttaa gttgccaacc tccccctccccca ataaaaattt acttacacct 240
cctgcctttg tagttcttgtt attcaacttta ctatgtgata gaagtagcat gttgctgcc 300
gaataacaagc attgcttttg gcaaattaaa gtgcgtgtca tttcttaata cactagaaag 360
ggggaaataaaa tttaaagtaca caagtccaaag tctaaaactt tagtactttt ccatgcagat 420
ttgtgcacat gtgagaggtt gtccagttt tctagtgatt gttattttaga gagttggacc 480
actattgtgt gt 492

<210> 303
<211> 470
<212> DNA
<213> Homo sapiens

<400> 303
tctggggcag caggtactcc ctacggcact agtctacagg gggaggacg ctctgtgctg 60
gcagcgggtgg ctcacatggc ctgtctgcac tgtaaccaca ggctggatg tagccaggac 120
ttggtctcct tggaaagacag gtctgtatgtt tggccaatcc agtccttcag accctgcctg 180
aaacttgtat ttacgtgaa cttaaagaat aaaatgcatt tctacccga tctcgcccc 240
aggactggca cgacaggccc acggcagatt agatcttttcc cagactgtca tcggtgctg 300
gaattccagc caccacttct gattcgattc cacagtgtac ctgtctctg agtattttaa 360
agaagccatt gtcacccag tcagtttcc aggagttggc aaccagccag taggggtgtgc 420
cattctccac tccccagccc aggtgcggc tggcatggac ctggcccgcg 470

<210> 304

<211> 79

<212> DNA

<213> Homo sapiens

<400> 304

tgtcccatcg ttaactcagc ctcaaatttc aactgtcagg ccctacaaag aaaatggaga 60
gcctttctg gtggatgcg 79

<210> 305

<211> 476

<212> DNA

<213> Homo sapiens

<400> 305

tcactgagcc accctacagc cagaagagat atgaggaaat tgttaaggaa gtcagcac 60
acattaagaa aattggctac aaccccgaca cagtagcatt tgcgcatt tctgggttgg 120
atggtgacaa catgctggag ccaagtgcata acgtaaatggg ctttcaagac catgttaaa 180
aagctctggg aatggcgatt tcatgttac acaaattggc atgcgtgtgt ttcaagatgc 240
ttggttcaag ggatggaaag tcaccctgtaa ggatggcaat gccagtggaa ccacgctgct 300
tgaggctctg gactgcatttcc taccaccaac tcgtccaact gacaaggccct tgccctgc 360
tctccaggat gtctacaaaa ttgggtggtaa gttggctgtaa aacaaatgg aatggatgtt 420
gatagagtac tgtctgcctt cataggttatt tagtatgtg taaatatccc taggtt 480

<210> 306

<211> 404

<212> DNA

<213> Homo sapiens

<400> 306

tctgtctcg agctcaggc gcagccagca cacacaggag cccacaggac agccacgtct 60
tcacagaaac tacagaagtcc aggaccagg cgaggaccc aggaacaagt gccccctgca 120
gacagagaga cgcagtagca acagttctg aacaactaca taataatgcg gggagaatcc 180
tgaagaccac tgcattccac aagcactgac aaccacttca ggattttatt tcctccactc 240
taaccccccag atccatttat gagaagtggatggc aggggcattgg agggtgaagg 300
gacagcaagg atggctctgag ggcctggaaa caatagaaaaa tcttcgtcct ttagcatatc 360
ctggactaga aaacaagagt tggagaagag ggggggttcat acta 404

<210> 307

<211> 260

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(260)

<223> n=A,T,C or G

<400> 307

tcctgcctan acatctgtga gggcctcaag ggctgtgcc tcgactttct ccctagctaa 60
gtccacccgt ccagggacac agccaggccca ctgctctgtg ctgacttcca ctgcagccaa 120
gggtcaaaat gaagcatctg cggaggccag gactccttgg catcgacac agtcagggga 180
aaagccaccc tgactctgca ggacagaggg tctagggtca tttggcagga gaacactgg 240
gtcccaaggg aagcnancat 260

<210> 308

<211> 449
<212> DNA
<213> Homo sapiens

<400> 308
tctgtgtcc cgactccccc atctcaggta ccaccgactg cactggcg ggccctctgg 60
ggggaaaggc tccacgggc agggatacat ctcgaggcca gtcatcctt ggaggcagcc 120
caatcaggta aaagattttg cccaaactggt cggcttcaga gtttccacag aagagaggct 180
ttcgcacgaaa catctctgca aagatacagc caaacactcca catgtccaca ggtgttgcatt 240
atgtggactg cagaagaact tcgggagctc ggtaccagag tgtaacaacc ttgatcgaaa 300
cggtctggcaa gcctgggtgg ggtgccttgtt ccagatatgt ccttaggtcc tggtctacat 360
gctcaaacac cagggttacc ttgatctccc ggtcagttcg ggtatgtggca cagacgtccca 420
tcagccggac aacattggga tgctaaaaa 449

<210> 309
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (384)
<223> n=A,T,C or G

<400> 309
ctgtggaaac ctgggggtgcc gggtaaatgg agaactccag cttggatttc ttgccataat 60
caactgagag acgttccatg agcaggagg tgaacctcaga accagttccc ccaccaaagc 120
tgtggaaaac caagaagccc tgaagaccgg tgcactggtc agccagctt cgaattcggt 180
ccaaacacaag gtcattatgtc tccttgccaa tggtgttagtg ccctcgggca tagttattgg 240
cagcatcttc cttgcctgtg atgagctgct cagggtggaa gagctggcg taggtgccag 300
tgcaacttc atcaatgact gtgggttcca agtctacaaa cacagccccgg ggcacgtgct 360
tgccagcgcc cgtctcactt gaanaagggt gtttgaagga agtcatctcc t 420

<210> 310
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (250)
<223> n=A,T,C or G

<400> 310
tcctcggtcca gcttgactcg attagtccctc ataaggtaag caaggcagat ggtggctgac 60
cgggaaatgc ctgcctggca gtggacaaac acccttcctc cagcatctt gatggagtct 120
atgaagtcaa tggcctcggtt gaaccaggag ctgatgtctg cttgtgggtt gtcctccaca 180
gggatgctct tggactggta gtgaccctca aaatggttgg gacaattggc tgagacgttg 240
atcaaggcan ttatgccccaa ggcattccagc atgtcccttgc gggaaagcgtg atacgcactg 300
cccaggtaca gaaagggcag 320

<210> 311
<211> 539
<212> DNA
<213> Homo sapiens

<400> 311
tctggccat gaagctgaag ttgggagaga tcatgttcg cctctgttc acaaactcaa 60
aggcctcg tcagcttgcg cgattagtcc tcataaggta agcaaggcag atggtggtc 120
accggaaat gcctgcctgg cagtggacaa acacccttcc tcacgttcc ttgtatggagt 180
ctatgaagtc aatggcctcg tgaaccagg agctgtatgtc tgccctgtgg ttgtcctcca 240
cagggatgt cttgtactgg tagtgaccct caaaatggtt ggacaattt gctgagacgt 300
tcatgtatccc agttatgtccc aaggcatcca gcatgtcctt gccccaaagcg tgatacggc 360
tgcggcggta cagaaaggc aggatccc ccggggcacc ctgaaatcca gaaatatccca 420
acattcatca agcttgctca aagccaaggc cagtggccat acccacaaaa actttctgtc 480
ggaaaagtca atttcagata ccgagtgaa tcagtttgt tgctggagga taaataaat 540

<210> 312
<211> 475
<212> DNA
<213> Homo sapiens

<400> 312
tcaaggatct tcctaaagcc accatgttagg aggattcgga cgagagtctg agctgtatgg 60
cagaccatgt cctgtgttc tagggtcatg actgtgtgtc ctctaaagtt gccactctca 120
caggggttcag tgataccac tgaacctggc aggaacagtc ctgcagccag aatctgc 180
cagcgcctgt atgcaacgtt tagggccaaa ggctgttgg tgggggttgg catcacagca 240
taatggccta gttagtcaag gatccaggggt gtgaggggct caaagccagg aaaacgaatc 300
ctcaagtctt tcagtagtct gatgagaact ttaactgtgg actgagaagc atttccctcg 360
aaccagcggg catgtcgat ggctgctaag gcactctgca atactttgtat atccaaatgg 420
atgtctggat ccagtttcg aagattgggt ggcactgttg taatgagaat cttca 480

<210> 313
<211> 456
<212> DNA
<213> Homo sapiens

<400> 313
tccacttaaaa gggtgccctt gccaactggg ggaatcatcg ccacttccag caccacgcca 60
agccctaacat cttccacaag gatcccgtat tgaacatgtc gcacgtgtt gttctggcg 120
aatggcagcc catcgagtac ggcaagaaga agctgaaaata cctgccttac aatcaccagc 180
acgaataactt cttccgtt gggccggccgc tgctcatccc catgtatttc cagtagccaga 240
tcatcatgac catgtcgat cataagaact gggtgaccc ggcctggcc gtcagctact 300
acatccgggtt cttcatcacc tacatccctt tctacggcat cctgggagcc ctccctttcc 360
tcaacttcat cagttccgt gagagccact ggtttgtgt ggtcacacag atgaatcaca 420
tcgtcatgga gattgaccag gaggacctcg gcccgc 456

<210> 314
<211> 477
<212> DNA
<213> Homo sapiens

<400> 314
tgcgtggct tctgaaagcc tggatctgga atcatttccacc agattattct gggaaaactat 60
gcgtaccctg gtgttcttct gattggcact gactcccaca ccccaatgg tggcggccctt 120
ggggggcatct gcattggagt tgggggtggc gatgtgtgg atgtcatggc tgggatcccc 180
tgggagctga agtggcccaa ggtgattggc gtgaagctga cgggtctct ctccgggttgg 240
tcctcaccat aagatgtat cctgaaagggt gcaaggcatcc tcacgggtgaa aggtggcaca 300
gggtgcaatcg tggaaatacca cggggcctggt gttagactcca tctctgtgcac tggcatggcg 360
acaatctgca acatgggtgc agaaattggg gcccacatt ccgtgttcccc ttacaaccac 420

aggatgaaga agtatcttag caagaccggc cgggaagaca ttgccaatct agctgat 477
<210> 315
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 315
caggtactgg atgtcaggtc tgcgaaaactt cttanatttt gacctcagtc cataaaaccac 60
actatcacct cggccatcat atgtgtctac tgtggggaca actggagtga aaacttcgg 120
tgctgcaggt ccgtggggaaa atcagtgacc agttcatcag attcatcaga atggtgagac 180
tcatcagact ggtgagaatc atcagtgtca tctacatcat cagagtcgtt cgagtcaatg 240
g 241

<210> 316
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 316
ntnttgtat agtgtggttt atggactgag gncaaaatnt aagaagttc gcagacctga 60
catccaancc tgcccngncg gnccgtcgaa aggnngaatt ctgcagatat ccatcacact 120
ggccggccgct cgagcatgca tctagagggc ccaattcgcc ctatantgag tnatattaca 180
attcactggc cgtcnntta caacgtcgtg actggggaaa ccctggcg 240
a 241

<210> 317
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 317
aggtaaccctg ctcancagcc tgggngcctg ggttgtctcc ttgtccatcc actggtccat 60
tctgctctgc attttttgt tcctctttg gaggttccac tttgggttg ggctttgaaa 120
ttatagggct acaantacct cggccgaaac cacnctaagg gcaattctg cagatatcca 180
tcacactggc ggnccgtcgaa gcatgcatct agagggccca attcgcccta tagtgagtcg 240
t 241

<210> 318
<211> 241

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 318
cgngnacaan ntacattgtt gganggtntg nggntctgan tntttantta cantggagca 60
ttaatatttt cttnaacgtn cctcacccctc ctgaantaaa nactctgggt ttagcgctc 120
tgtgctnana accacntnaa ctttacatcc ctcttttggaa ttaatccact gcgcggccac 180
ctctgccgacc accacgctaa gggcnaattc tgcatgatc catcacactg gcccggcgtc 240
n
241

<210> 319
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 319
caggtactga tcgggtgcgtg gaantccagc caccantntt gattcgattc cacagtgate 60
ctgtccctctg agtattttaa agaagccatt gtcaccccaag tcagtgttcc aggagttggc 120
aaccaggccag tagggtgtgc cattctccac tccccagccc aggatgcgga tggcatggcc 180
accatcatc tctccgggtga cgtgttggta cctcggccgc gaccacgcta agggcgaatt 240
C
241

<210> 320
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 320
ggcaggtacc aacagagctt agtaatntct aaaaagaaaa aatgatcttt ttccgacttc 60
taaacaagtg actatactag cataaatcat tctagtaaaa cagctaaggat atagacattc 120
taataatttg gaaaaaccta tgattacaag tgaaaaactca gaaatgc当地 gatgttgggt 180
ttttgtttct cagtcgtctt tagctttaa ctctnnnaan cncatgcaca cttgnactc 240
t
241

<210> 321
<211> 241
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 321
angtaccaac agagcttagt aattnntaaa aagaaaaaat gatcttttc cgacttctaa 60
acaagtgact atactagcat aaatcattct agtaaaacag ctaaggata gacattctaa 120
taatttggga aaacctatga ttacaagtga aaactcgaaa atgcaaagat gttggtttt 180
tgttcttag tctgcttag cttaactc tggaagcgca tgcacacntg aactctgctc 240
a 241

<210> 322
<211> 241
<212> DNA
<213> Homo sapiens

<400> 322
ggtaccaaca gagcttagta atttctaaaa agaaaaaatg atctttcc gacttctaaa 60
caagtgact tactagata aatcattctt ctagtaaaac agctaaggta tagacattct 120
aataatttgg gaaaacctat gattacaagt aaaaactcgaa aaatgcaaag atgttggttt 180
tttggttctc agtctgctt agctttaac tctgaaagcg catgcacact gaactctgct 240
c 241

<210> 323
<211> 241
<212> DNA
<213> Homo sapiens

<400> 323
cgaggtactg tcgtatccctc agccttggtc tatttcttta ttttagctt acagagatta 60
ggtctcaagt tatgagaatc tccatggctt tcaggggcta aactttctg ccattcttt 120
gctttaccg ggctcagaag gacatgtcag gtgggatacg tttctctt tcagagctga 180
agaaagggttc tgagctgcgg aatcagtaga gaaagcctt gtcgtactga ctccctggct 240
t 241

<210> 324
<211> 241
<212> DNA
<213> Homo sapiens

<400> 324
aggtaactgtc gtatcctcag cttgttcta tttctttatt ttagcttac agagattagg 60
tctcaagttt tgagaatctc catggcttcc aggggctaaa cttttctgcc attctttgc 120
tcttaccggg ctcagaagga catgtcaggt gggatacgtg tttctcttcc agagctgaag 180
aaagggtctg agctgcggaa tcagtagaga aagccttggc ttcgtactgc cttggctt 240
C 241

<210> 325
<211> 241
<212> DNA
<213> Homo sapiens

<400> 325
ggcaggtaca tttgtttgc ccagccatca ctcttttttg tgaggagcct aaatacatcc 60
ttcctgggtt ccagagtccc cattcaaggc agtcaagttt agacactaac ttggcccttt 120

cctgatggaa atatccctc catagcagaa gttgtttct gacaagactg agagagttac 180
atgttggaa aaaaaaagaa gcattaactt agtagaactg aaccaggagc attaagtct 240
g 241

<210> 326
<211> 241
<212> DNA
<213> Homo sapiens

<400> 326
gcaggtacat ttgtttgcc cagccatcac tctttttgt gaggagccta aatacattct 60
tcctggggtc cagagtcccc attcaaggca gtcaagttaa gacactaact tggcccttc 120
ctgatggaaa tatttcctcc atagcagaag ttgtgttctg acaagactga gagagttaca 180
tgttggaaa aaaaagaagc attaacttag tagaactgtat ccaggagcat taagttctga 240
a 241

<210> 327
<211> 241
<212> DNA
<213> Homo sapiens

<400> 327
ggtaccagac caagtgaatg cgacagggaa ttatttcctg tggtgataat tcatgaagta 60
gaacagtata atcaaaaatca attgtatcat cattagttt ccactgcctc acactgtga 120
gctgtgcca gtagtagtgt gacacctgtg ttgtcatttc ccacatcagc taagagcttc 180
caaggaaagc ccaaattccag atgagtctca gagagggatc aatatgtcca tgattatcag 240
g 241

<210> 328
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)..
<223> n = A,T,C or G

<400> 328
ggtacnagac caaatgaang ccacagggaa ttatttcctg tggtgataat tcatgaagta 60
gaacantata atcaaaaatca attgtatcat cattagttt ccactgcctc acactgtga 120
gctgtgcca gtagtagtgt gacacctgtg ttgtcatttc ccacatcagc taagagcttc 180
caaggaaagc ccaaattccag atgagtctca gagagggatc aatatgtcca tnatcatcan 240
g 241

<210> 329
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

100

<400> 329
ttcaggtcga gttggctgca gatttgtggt gcnttctgag ccgtctgtcc tgcgccaaaa 60
ngttcaag tattataaa aacatatgga tccccatgaa gccctactac accaaagttt 120
accaggagat ttggatagga atggggctga tgggcttcat cgtttataaa atccgggctg 180
ctgataagaa gtaaggctt gaaagcttca gcgcctgctn ctggtcanna ctaaccatan 240
n 241

<210> 330
<211> 241
<212> DNA
<213> Homo sapiens

<400> 330
tttgtgcag atttgtggtg cgttctgagc cgtctgtcct gcgc当地 60
attattaaaa acatatggat ccccatgaaag ccctactaca ccaaagtta ccaggagatt 120
tggataggaat tggggctgtat gggcttcatc gtttataaaa tccgggctgc tgataaaaaga 180
agtaaggctt tgaaagcttc agcgcctgct cctggtcatc actaaccaga ttacttgaa 240
g 241

<210> 331
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 331
nttttaggna ctttgggctc cagacttcac tggtcttagg nattgaaacc atcacctggn 60
ntgcattcct catgactgag gttaacttaa aacaaaaatg gtaggaaagc tttcctatnc 120
ttcnggtaaag anacaaatnt nctttaaaaa aangtggaaag gcatgacnta cgtgagaact 180
gcacaaaactg gccactgaca aaaatgaccc ccatttgtgt gacttcattg agacacatta 240
c 241

<210> 332
<211> 241
<212> DNA
<213> Homo sapiens

<400> 332
tgtgaggaga gggAACATGC tgagaaaactg atgaagctgc agaaccaacg aggtggccga 60
atcccttc aggatatcaa gaaaccagac tgtgatgact gggagagcgg gctgaatgca 120
atggagtgtg cattacattt ggaaaaaaaaat gtgaatcagt cactactgga actgcacaaa 180
ctggccactg acaaaaaatga ccccccatttg tgtgacttca ttgagacaca ttacctgaat 240
g 241

<210> 333
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1) ... (241)
<223> n = A,T,C or G

<400> 333
caggtacaag cttttttttt tttttttttt ttgnaaaatac tnnttattgn 60
aaatattcta tcctaaaattc catatagcca attaattntt acanaatntt ttgttaattt 120
ttgngngtat aaattttaca aaaataaagg gtatgttgt tgacacacaac ttacaaataa 180
taataaaactn ttattnnaa atattnnta ttgnaaaatat tctttatcct aaattccata 240
t 241

<210> 334
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (241)
<223> n = A,T,C or G

<400> 334
tacctgctgn aggggntgaa gncntctctg ctgccccagg catctgcanc ccctgctgct 60
ggttctgccc ctgctgcagc agaggagaag aaagatgaga agaaggagga gtctgaagag 120
tcagatgatg acatgggatt tggcctttt gattaaannc ctgctccct gcaaataaag 180
ccttttaca caaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aagcttgtac ctgcccnggc 240
g 241

<210> 335
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1) ... (241)
<223> n = A,T,C or G

<400> 335
ctatgtgctg ggatgactat ggagacccaa atgtctcana atgtatgtcc cagaaacctg 60
tggctgcttc aaccattgac agttttgctg ctgctggctt ctgcagacag tcaagctgca 120
gctcccccaa aggctgtct gaaacttgag ccccggtgga tcaacgtgct ccaggaggac 180
tctgtgactc tgacatgcc aggggctcgc agccctgaga gcgactccat tcagtggttc 240
c 241

<210> 336
<211> 241
<212> DNA
<213> Homo sapiens

<400> 336
taccaaccta tgcagccaag caacccatc agttccatc aaggccaccc ctaccacaaac 60
cgaaagtatc atctcaggaa aacttaattc ctgccccgtcc tgctcctgca cctcctttat 120
atagttccct cacttgattt ttttaacctt ctttttgcaat atgtcttcag ggaactgagc 180
taataactttt tttttctt atgtttctt gaaaagcctt tctgttgcaa ctatgaatga 240
a 241

<210> 337
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 337
ggtaactgtat gtagctgcac tacaacagat tcttaccgtc tccacanagg tcataanattg 60
taaatggtna atactgactt ttttttatt cccttgactc aagacagcta acttcatttt 120
cagaactgtt tttaaaccttt gtgtgctggt ttataaaaata atgtgtgtaa tccttggc 180
tttcctgata ccagactgtt tcccgtggtt ggtagaata tatttgntt tgatgcttat 240
a 241

<210> 338
<211> 241
<212> DNA
<213> Homo sapiens

<400> 338
aggtagcagg gtgcgctgag ccgagtttac acggaaaggaa taaagccccat ttagtttctt 60
ctcaaatggta gttttccact ttcccttggaa gtagacagca tccaccagga tcatacctgg 120
atccccatct acagaacctt caggtAACAA gtttgggatt ttgccttgg tttgagtctt 180
gaccaggaa ttaatctttt ttctagcttc ttctgcacat tcttagaaat ctactgcctg 240
g 241

<210> 339
<211> 241
<212> DNA
<213> Homo sapiens

<400> 339
tacccgacggc tcctgggggg agagagtgaa gggacacggg aagaatcaaa gtcgagcatg 60
aaagtgtctg caactccaaa gatcaaggcc ataaccagg agaccatcaa cggaagatta 120
gttcttggc aagtgaatga aatccaaaag cacgtatgg accaatgaaa gttccgcct 180
gttgtaaaat ctatTTTCCC ccaaggaaag tccttgcaca gacaccagtg agtgagttct 240
a 241

<210> 340
<211> 241
<212> DNA
<213> Homo sapiens

<400> 340
gtagccctca cacacacatg cccgtAACAG gatttatcac aagacacgcc tgcatgtaga 60
ccagacacag ggcgtatgga aagcacgtcc tcaagactgt agtattccag atgagctgca 120
gatgtttacc taccacggcc gtctccacca gaaaaccatc gccaactcct gcgatcagct 180
tgtgacttac aaaccttggtt taaaagctgc ttacatggac ttctgtcctt taaaagcttc 240
c 241

<210> 341

<211> 241
<212> DNA
<213> Homo sapiens

<400> 341
gtaccgccta ctttcgtctc atgtctccga acttcttgct gatggccgtt ccaacgttgc 60
tggaaagctgc agttgccttt tgccctgcgt gactcaggggt ttcatgtgtt ttcttgttagg 120
cagtggtagt ctgcatagtca tgccagcttt tgctgaaggta ctgttttaat tcattcatca 180
ggttcatgcc gagttttgtt ttatctcaac tagatgcctt tctttcgctg aaaaaacttg 240
t 241

<210> 342
<211> 241
<212> DNA
<213> Homo sapiens

<400> 342
gtacattgggt gctataaaata taaaatgtcac ttatgaagca tgaaaattaag cttctttttt 60
cttcaaggtt tttctcttgt ctagcaatct gttaggcttc tgaaccaaga ccaaataatgtttt 120
acgttcctct gctgcataacc aacgttactc caaaacaataa aaatctatca tttctgctct 180
gtgctgagga atggaaaatg aaaccccccac cccctgaccc ctaggactat acagtggaaa 240
c 241

<210> 343
<211> 241
<212> DNA
<213> Homo sapiens

<400> 343
gtacatgtgg tagcagtaat ttttttgaag caactgcact gacattcatt tgayttttct 60
ctcattatca gattctgttc caaacaagta ttctgttagat ccaaataatggat taccagtgtg 120
ctacagactt cttattatag aacagcattc tattctacat caaaaatagt ttgtgtaaatg 180
tagtttttgtt taccatctaa aatattttta aatgttcttt acataaaaaat ttatgttgtg 240
t 241

<210> 344
<211> 241
<212> DNA
<213> Homo sapiens

<400> 344
ggtacaaaaat tgttggaaatt tagctaatacg aaaaacatag taaaatattta caaaaacgtt 60
gataaacatta ctcaagtcac acacatataa caatgttagac aggtcttaac aaagtttaca 120
aattgaaattt atggagattt cccaaaatga atctaatacg tcattgctga gcatggttat 180
caatataaca tttaagatct tggatcaaattt gttgtccccg agtcttctgc aatccagtc 240
t 241

<210> 345
<211> 241
<212> DNA
<213> Homo sapiens

<400> 345
ggtacgaagc tgagcgcacg ggggttgcac cagcgtggag cctggacctc aaacttcacg 60
gaaaatgctc tctctcttttgc acaggcttcc agctgtctcc taatttcctg gatgaactct 120

ccccggcgat ttaactgatc ctgaaaagtg gtgagaggac tgaggaagac aaccaggta 180
gcgttagatc ggcctctgag ggtggtgc 240
g 241

<210> 346
<211> 241
<212> DNA
<213> Homo sapiens

<400> 346
cagttaccac tgaggctgag atggggatga gggcagagag agggggagccc cctcttccac 60
tcagttgttc ctactcagac tggcactc taaacctagg gaggttgaag aatgagaccc 120
ttagggttta acacgaatcc tgacaccacc atctataggg tcccaacttg gttattgttag 180
gcaacccctcc ctcttcctt ggtgaagaac atcccaagcc agaaagaagt taactacagt 240
g 241

<210> 347
<211> 241
<212> DNA
<213> Homo sapiens

<400> 347
aggcacatct aaaggcatga agcactaat tggcaatta acattagtgt ttgttctctg 60
atggtatctc tgagaataact gggtttagga ctggccagta gtgccttcgg gactgggttc 120
acccccaggct cgccggcagt tgtcacagcg ccagccccgc tggcctccaa agcatgtgca 180
ggagcaaatg gcaccgagat attccctctg ccactgttct cctaegtggt atgtcttccc 240
a 241

<210> 348
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 348
angtacttgg caagattna tgctttngn ctcantgaca tcattcataa cttgttnngtg 60
tgancagagg aggagnncat catcnntgtcc tcattcgtca gnnncctctc ctctctgaat 120
ctcaaacaag ttgataatgg agaaaaattt gaattctcag gattgaggct ggactgggtc 180
cgccctacang catacactag cgtggctaag gcccctctgc accctgcata anaaccctga 240
c 241

<210> 349
<211> 241
<212> DNA
<213> Homo sapiens

<400> 349
gcaggttacca ttgtctgac ctctgtaaaa aatgtgatcc tacagaagtg gagctggata 60
atcagatagt tactgctacc cagagaata tctgtgatga agacagtgt acagagacct 120
gctacactta tgacagaaaac aagtgttaca cagctgtggt cccactcgta tatggtggtg 180
agacaaaaat ggtggaaaca gccttaaccc cagatgcctg ctatcctgac taatttaagt 240

105

c

241

<210> 350
<211> 241
<212> DNA
<213> Homo sapiens

<400> 350
aggtaactgtg gatatttaaa atatcacagt aacaagatca tgcttggcc tacagtattg 60
cgggccagac acttaagtga aagcagaagt gtttgggtga ctttcctact taaaattttg 120
gtcatatatcat ttcaaaacat ttgcattctg gtggctgca tatgcttcc tattgatccc 180
aaaccaaatac tttagaatcac ttcatattaaa atactgagcg gtattgaata ctgcgaagca 240
g 241

<210> 351
<211> 241
<212> DNA
<213> Homo sapiens

<400> 351
tacagaaaatc atttggagcc gtttgagac agaagttagag gctctgtcaa gtcaataactg 60
cattgcagct tggccactg aagaagccac gcctgagata caaaagatgc actacacttg 120
accgcctta tggcgcttc ctctccccctt ctctctcatc aactttatta ggttaaaaaca 180
ccacatacag gtttctcca aatgactccc tatgtctggg gtttggtag aattttatgc 240
c 241

<210> 352
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 352
gtaccctgtn gagctgcacc aagattannt gggccatca tgactgcanc cacnacgang 60
acgcaggcgt gnagtgcac tcgtctgacccg gaaaccctt cacttctctg ctcccgaggt 120
gtcctcnngc tcataatgtgg gaaggccanan gatctctgan gagttncctg gggacaactg 180
ancagcctct ggagaggggc catataaaa gctcaacatc attggcaaaa aaaaaaaaaa 240
a 241

<210> 353
<211> 241
<212> DNA
<213> Homo sapiens

<400> 353
aggtaaccaggc gcattaattt gggcaaggaa agtgtcataa tttgatactg tatctgtttt 60
ccttcaaagt atagagctt tggggaaaggaa aagtattgaa ctgggggttg gtctggccta 120
ctggggctgac attaactaca attatggaa atgcaaaaagt tggggata tggtagtgc 180
tggggatattt ttcaaggta ttaataata attaaaaact actataaaaa 240
c 241

<210> 354
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 354
ngcaggtccg ggcaggtacc aagattcatt ctcatcaaaa actagaaaaca gaaggc 60
ttccagtttc cttctggat tgaatacttt caagtaaggt ctgcacaaa caatcagg 120
gccaattaat ccactgtaga ggtccctaac ttgatccaca gttgaataat aagccc 180
aatacaagca gaatcctctg ttccagctcc agatcttct gggatttcc atacgt 240
g 241

<210> 355
<211> 241
<212> DNA
<213> Homo sapiens

<400> 355
ggtacccacc ctaaatttga actcttatca agaggctgat gaatctgacc atcaaatagg 60
ataggatgga ccttttttg agttcattgt ataaacaaat tttctgattt ggacttaatt 120
cccaaaggat taggtctact cctgctcatt cactcttca aagctctgtc cactctaact 180
tttctccagt gtcataagata gggatttgct cactgcgtgc ctatcttcc ttca 240
t 241

<210> 356
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 356
aggtaactgta attgagcatc cggaaatntgg agaagtaatt tagctacagg gtgaccaacg 60
caagaacata tgccagttcc tcgttagagat tggactggct aaggacatc agctgaaggt 120
tcatgggttt taagtgcctt tggctcactg aagcttaagt gaggattcc ttgcaatgag 180
tagaaattcc cttctctccc ttgtcacagg tttaaaaacc tcacagctt tataatgtaa 240
C 241

<210> 357
<211> 241
<212> DNA
<213> Homo sapiens

<400> 357
tttgtacca ccgatatgat caaggaaaat tctgcccatt tttatggctg aagttctaaa 60
aacctaattc aaagttcttc catgatccta cactgcctcc aagatgtcc aggctggcat 120
aaggcctgag cggcggtgag atcccgccgctt gccagcagct tgcgcctt cagctggat 180

gaagccccctc ggccacccga gtctccagga cctgccccggg cgccgctcga aaggggcgaat 240
t 241

<210> 358
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 358
aggtacgggg agtgggggtg aagcntgttc tctacatagg caacacagcc gcctaantca 60
caaagtcaagt ggtcgccgcg ttcgaccaac atgtggtagg cattccacgg ggcgtatgaag 120
tctgggtgct gtgcgtcgagt ctctgaatat tttgatagga agcgacaaga aaattcaaac 180
tgctcttgc tgactactgg aaagtggaaaa gatgctcaag ttaccattc aaagaaacca 240
t 241

<210> 359
<211> 241
<212> DNA
<213> Homo sapiens

<400> 359
gaggtacaca aaaggaatac cttctgagag ccagggagtg agggaaagggg aaggagactt 60
gacgtcaagg gtgccttta ggaacatgac gggccagcca gcctgcggccaa actttgaggc 120
cctgctgggc tcttgtact ataaatatac tgtctatattc taatgcaatc cgtctttcc 180
gaaagatctt gttatctttt actattgaga catgctttca tttttgtggt cctgtttcca 240
a 241

<210> 360
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 360
ngtactctat actaattctg ctttttata ctttaattcta aatttctccc ctctaattta 60
caacaaattt tgtgatttt ataagaatct atgcctcccc aatttctcaga ttcttctctt 120
ttctccctta tttcttgct taaattcagt ataagcttca ttggatattt aggcttcatg 180
cacattctta ttcctaaaca ccagcagtcc ttcagagacc taaaatccag tataggaata 240
a 241

<210> 361
<211> 241
<212> DNA
<213> Homo sapiens

<400> 361

aggtactctc cgtccccga cactgaacat tatccagcca gatctgccc gtgccagctc 60
ccactttgtta cttttcttac tattctgtct agaatcatgt ctatgattt taacagatat 120
agaaccactc ctagaaaatg ttcttcact ttctcgttc ctttttaatc tatcatcctg 180
actactgaac ttaaaatctt tttcttcctt ttttggttc tctttcttt tatcctgttc 240
a 241

<210> 362
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 362
aggtactttt atacctngct tangtcagtg acagattac caatgacaac acaattttaa 60
aattccaaca catatattac tttgtcctat gaaggcataa aagtcaatat attttaaattt 120
ttaaaaaacag aatggatata atgaccttt tacacatcag tgatattaa aagacttaaa 180
gagacaatac tatggtagg acactggctt cctattccag ccctaattaa agaaaaaaata 240
g 241

<210> 363
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 363
ttangtacta aaaacaaaaat cctaattctg ttttaaagag ctgggagatg ttaatcatat 60
gctcagtttt tccacgttat aatttcctaa atgcaaactt ttcaatcagg gcagttcaaa 120
ttcattacat cacagtaaat aacagtagcc aactttgatt ttatgcttat agaaaaaaaaa 180
atcctgtaga tataaaaaaca gcaaattttg acaaataaaaa ctcaaaccat tcatccctaa 240
a 241

<210> 364
<211> 241
<212> DNA
<213> Homo sapiens

<400> 364
ggtacaagca gtttagtcctg aaggccccctg ataagaatgt catcttcctcc ccactgagca 60
tctccaccgc cttggcccttc ctgtctctgg gggccccataa taccaccctg acagagattc 120
tcaaaggcct caagttcaac ctcacggaga cttctgaggc agaaatttcac cagagcttcc 180
agcacctcct gcgcaccctc aatcagtccca gcgatgagct gcagctgagt atgggaaatg 240
c 241

<210> 365
<211> 241
<212> DNA

<213> Homo sapiens

<400> 365

cgaggtactg agattacagg catgagccac cacgcccggc caaaaacatt taaaaaatga 60
ctgtccctgc tcaaatactg cagtagaaaa tgtaatttga catatatcac ttccagaaaa 120
aaatttaaa tctttctata aaatgaattt gatacatcat cagcatgaag tgaagttaaa 180
atctcttaca aagtaaattc aggtatatca acaatgagat ccaaaagtat cggttcaaga 240
t 241

<210> 366

<211> 241

<212> DNA

<213> Homo sapiens

<400> 366

ggcaggtaca catcaaacac ttcattgcct aaatgcaggg acatgcttcc atctgaccac 60
ttgactatcc gagcattgct ttcttaatt tcatttcctt cttcatctcg gcttatcctc 120
catcttatacg tattttctac cttaatttt aacctggttc taccttcttc atccagcatt 180
tcttcatctt caaattcatc ttcataatac tgggctctac acttgagaaa gttgggcagt 240
t 241

<210> 367

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(241)

<223> n = A,T,C or G

<400> 367

gcaggtacaa ataattccctg ttgtacatt tagtggacgc gattatctgt atacctcaaa 60
ttttaatttta agaaagtatc acttaaagag catctcattt tctatacgatt gaggcttaat 120
tactgaaaag tgactcaacc aaaaagcaca taaccttttta aaggagctac acctaccgca 180
gaaagtcaaga tgcctctgtaa ataactttgg tctttcaaaa tagtggcaat gcttaagata 240
c 241

<210> 368

<211> 241

<212> DNA

<213> Homo sapiens

<400> 368

tttgtacatt gttaatagtg accctcgag gaaatggatt tctttcttat taaaaactct 60
atggtatata agcattacat aataatgcta cttaccacc tttgtctca agaattatca 120
ccaaagtttt ctggaaataa gtccacataa gaattaaata tttaaaaggt gaaatgttcc 180
ttattttaac tttagcaaga tctttcttt ttcattaaga aacactttaa taatttaaa 240
g 241

<210> 369

<211> 241

<212> DNA

<213> Homo sapiens

110

<400> 369
gcaggtactt tattcttatt tcttatccta tattctgtgt tacagaaaaa ctactaccat 60
aaacaaaaca ccaaccagcc acagcagttg tgtcaagcat gacaattggc ctatcttca 120
cattttatta gtaagtctat caagtaagag atgaagggtc tagaaaaacta gacacaaagc 180
aaccagggtc caaatcacca aggttagatct gtgccttagct aaaggaaac acccgaaagat 240
t 241

<210> 370
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 370
ngttcacagt gccccctccgg cctcgccatg aggctcttcc tgtcgtccc ggtccctggtg 60
gtggttctgt cgatcgctt ggaaggcccc gccccagccc agggggacccc agacgtctcc 120
agtgccttgg ataagctgaa ggagtttggaa aacacactgg aggacaaggc tcgggaactc 180
atcagccgca tcaaacagag tgaactttct gccaaatgc gggagtgggtt ttccagaagac 240
a 241

<210> 371
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 371
ggcaggtcat cttgagcctt gcacatgata ctcagattcc tcacccttgc ttaggagtaa 60
aacaatatac tttacaggg gataataatc tccatagttt tttgaagtgg ctgtaaaaag 120
gcaagattga cttttatgac attggataaa atctacaaat cagccctcga gtattcaat 180
gataactgac aaactaaatt atttccctag aaaggaagat gaaaggagnat ggagtgtgg 240
t 241

<210> 372
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 372
aggtacagca aagcgaccct tggtggnata gatcagacgg aaattctctc ccgtcttgnc 60
aatgctgatg acatccatga atccagcagg gttaggttata tcagtcgga ctttgcac 120
gattttaatg aaccgctgca tgcaaatttca ctttacttca tctcctgtca gggcataactt 180

aagtctgttc ctcaaggaaaa tgcgtgggg gagacactct ctcaacttgt ggggaccggt 240
g 241

<210> 373
<211> 241
<212> DNA
<213> Homo sapiens

<400> 373
tactgaaaca gaaaaaatgt attccacaa aagctgtac acagcggttt cccgtcccc 60
gaagcagtag aaaatcttag cattccaatg gaaggcatgt atttgtaaaa tattctaaaa 120
tcagctctat agtttccttg tcctcttga taaggatca gacagagggt gtgtccccct 180
tcagcagcta cccttcttga caaactggtc tccaataata cctttcagaa acttacaaga 240
c 241

<210> 374
<211> 241
<212> DNA
<213> Homo sapiens

<400> 374
caggtactaa aacttacaat aaatatcaga gaagccgtta gtttttacag catcgctgc 60
ttaaaaagcta agttgaccag gtgcataatt tcccatcagt ctgtccttgt agtaggcagg 120
gcaatttctg ttttcatgat cggaataactc aaatatatcc aaacatctt ttaaaaactt 180
gatttatagc tcctagaaag ttatgtttt taatagtcac tctactctaa tcagggctag 240
c 241

<210> 375
<211> 241
<212> DNA
<213> Homo sapiens

<400> 375
aggtacaaaag gaccagtatc cctacctgaa gtctgtgtgt gagatggcag agaacggtgt 60
gaagaccatc acctccgtgg ccatgaccag tgctctgccc atcatccaga agctagagcc 120
gcaaattgca gttgccaata cctatgcctg taaggggctca gacaggattg aggagagact 180
gcctattctg aatcagccat caactcagat tggccaaat gccaaaggcg ctgtgactgg 240
g 241

<210> 376
<211> 241
<212> DNA
<213> Homo sapiens

<400> 376
ggtacatttt actttccttc tttcagaatg ctaataaaaaa acttttgtt atactaaaaa 60
aaaccataaa tcagacaaaac aaaagaaaacg attccaacat cacttctgtg atgagaaaag 120
aggcaatgga attcaacata agcaaagaaa actctacctg gaggaaagaa atcgatcgc 180
gaagaaaacaa ctggggctg ctgccagact gcaggccatg cgaggaggag cttccctagag 240
g 241

<210> 377
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 377
tcctttctgt ccaggtgatt cacagactag acctttctta tcctcctcct agagtttga 60
cttgggactc tagtgttaag atgatgagcc cgtgcatacg gtcctctgc actttggtgg 120
aagtctccca gggtaggtt cctatttcaa acagtggaaat catgttcca gtgataaagt 180
ttaatgacct catcctttt ttttttttc tcatctgcca tttgtgtgc ttanatgggt 240
t 241

<210> 378
<211> 241
<212> DNA
<213> Homo sapiens

<400> 378
aggcagcga tcaggtcctt tatgggcagc tgctggcag ccccacaagg ccagggccag 60
ggcactatct ccgcgtcgac tccactcagc ccctcttggc gggcctcacc cccagcccc 120
agtccatatga gaacctctgg ttccaggcca gcccccttggg gaccctggta accccagccc 180
caagccagga ggacgactgt gtctttggc cactgctcaa cttccccctc ctgcagggga 240
t 241

<210> 379
<211> 241
<212> DNA
<213> Homo sapiens

<400> 379
tacggagcaa tcgaagagggc atatccacac ttgggggtggc tatagggctg gaaaatgctg 60
aagatgactg ctttcactga ggtcaaggat tgtaatatttgc ccagcttgc aaagccatta 120
aagcagaagt ttcttcagtg atcttctctc taagaaaacac catcacccatcc atgtgcctta 180
cagaggcccc ctgcgttctg ctgcattgtcttgc tttgcgcaat cccttgatga tgaagatgg 240
c 241

<210> 380
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 380
acgtacacgc agaccgacat gggnnnttca ggcntnagat caaactcaaa acctgnaatg 60
atatccactc tctttttctt aagctcaggg aatatttcca agttagaaatgc canaaagtca 120
tcggctaana tgcttcngaa tttgaattca tgcacatagg ccttggaaaaa actgtcaaac 180
tgannctgat cacccaccaa gtgggcnntn tatgacaccaa agcagaaaacc ttttcntan 240
g 241

<210> 381

<211> 241
<212> DNA
<213> Homo sapiens

<400> 381
aggatacaact taatggatta gctttgggt ttaactgaat atatgaagaa attgggtctg 60
tctaaagaga gggtatttca tatggctttt agttcacttg tttgtatttc atcttgattt 120
tttctttgg aaaataaaagc attctatttg gttcagattt ctcagattt aaaaaggctc 180
tatctcagat gtagtaaattt atttcccttc agtttgtgaa agcaggattt gactctgaaa 240
g 241

<210> 382
<211> 241
<212> DNA
<213> Homo sapiens

<400> 382
gtactgctat aatcaatacg tctgatagac aggtttatcc actatattga ccctacctct 60
aaaaggattt tcataaatttata tatgttttat gtttacacctt atgatacagt tgccctggaa 120
cacaaaaattt ttcatgtttaa ttaaaaaaaaag aagagttgtg cagacagaag aaatcaaattc 180
taagaaaaatc acaggaggtag ataaataactc tagaattcat atacccttgg aagatgggtt 240
t 241

<210> 383
<211> 241
<212> DNA
<213> Homo sapiens

<400> 383
ggcaggtaca aagtcttctc tttgtttttt ataattttaa agcaaataac acatttaact 60
gtatTTTaaGT ctgtgcaaat aatccttcag aagaaatatac caagattctg tttgcagagg 120
tcattttgtc tctcaaagat gattaaatga gttcgtcttc agataaagtg ctctgtcca 180
gcagaactca aaaggccttc aagctgttca gtaagtgttag ttcagataag actccgtcat 240
a 241

<210> 384
<211> 241
<212> DNA
<213> Homo sapiens

<400> 384
ggtacacaaaa atacacttgc aagcttgctt acagagacct gttaaacaaa gaacagacag 60
attctataaaa atcagttata tcaacatata aaggagtgtg attttcagtt tgTTTTTTta 120
agtaaatatg accaaactga ctaaataaga aggcaaaaca aaaaattatg cttcccttgac 180
aaggcctttg gagtaaacaa aatgctttaa ggctcctgggt gaatgggtt gcaaggatga 240
a 241

<210> 385
<211> 241
<212> DNA
<213> Homo sapiens

<400> 385
ggcaggtcta caatggctct gtcccttctg tggaaatcggtt acaccaagag gtctcagtcc 60
tggccctga cccccacagtg agctgttttag atgatccctt acatcttccct gatcaactgg 120

aagacactcc aatcctcagt gaagactctc tggagccctt caactctctg gcaccaggta 180
ggtttgagg ctatgtccct ttaacttatac catgcagagt agccaaactt tacctgaaaag 240
a 241

<210> 386
<211> 241
<212> DNA
<213> Homo sapiens

<400> 386
aggcaccttt ttccctctcca aaggaacagt ttctaaaggt ttctgggggg aaaaaaaaaact 60
tacatcaaat ttaaaccata tgtaaaactg catatttagtt gtgttacacc aaaaaattgc 120
ctcagctgat ctacacaagt ttcaaaagtca ttaatgcttg atataaattt actcaacatt 180
aaatttatctt aaatttattaa ttaaaaaaaaaa aactttctaa gggaaaaata aacaatgt 240
g 241

<210> 387
<211> 241
<212> DNA
<213> Homo sapiens

<400> 387
accccactgg ccgctgtgga gatatctccac tctccctcg tgagggccgc tccccccgac 60
cagtcgaact ttcgtaaatg gagttaatgt gtttccactc ccctttccc ctttctggcc 120
tttggtcca gaatttcctg gccttccggc atatcctggg agtccctcgac ttccaggaaa 180
gccaatttgct ccccgatcac cttaagacc cggaggacct attggacctg gaaatcctcg 240
t 241

<210> 388
<211> 241
<212> DNA
<213> Homo sapiens

<400> 388
tttgtactct tgtccacagc agagacattt agtataccat tggcatcaat gtcaaaagt 60
acttcaatct gaggaacacc tcggggtgca ggaggtatgc ctgtgagttc aaacttgcca 120
agcaggttgt tatcctttgt catggcacgc tcgccttcat aaacctgaat aagtacacca 180
ggctgggtgt cagaataggt agtgaaggctc tgtgtctgct tggtaggaat ggtggattt 240
c 241

<210> 389
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 389
tacccntggtt agtgaggacc ttgtcttnng tgcttatntc tttaagataa atacatggaa 60
ggatgtgaaa atcggAACAC caactatgtg tctcaactgca tctaagtgaa gcagccacag 120
ctgtgagagt ttcaaaagca gaaagatgt gatgtgaccc ctggaattca gacatactga 180
gctatgggtc agaagtgttt tactttaaaaa gcaaaacaatc cccagggaaat actgaatagg 240

a

241

<210> 390
<211> 241
<212> DNA
<213> Homo sapiens

<400> 390
gcaggtacat ccacatgtc ctccaaatga cgtttgggt cctgctgcc aacattctt 60
attgccagct gttcagggt catcttatct tcttcttcra cagccttatt gtaattctg 120
gctaattcca acatctctt taccactgat tcattgcgtt tacaatgttc actgttagtcc 180
tgaagtgtca aaccttccat ccaactcttc ttatgcaa at ttagcaacat ctctgttcc 240
a 241

<210> 391
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 391
cnngcacaan cttntgtttt tnntnntttt ttttttttn tctttattnn tttttantnt 60
taaanaaaaa nnntannnaa annngggttt aaatnctn nncagancat taaaactgaa 120
ggggaaaaaaaa aaacaaaaaa cgagcttntt anttnacntg ggnttggnn gntgctgatn 180
tnaagaagca annttan an cnngcnnnat ganngagnn tcannttgaa atttnnaccc 240
t 241

<210> 392
<211> 241
<212> DNA
<213> Homo sapiens

<400> 392
gaggtactaa atggtatcct tagattaaaa ttttgtgctt gataacagct gtttttct 60
cattagaaat aagatgccac acaaggaact acattccaga tttaaagaaaa tgaaaggata 120
ccattagtgt gtataacaga ttattgttca tacttgtaaa gcatcttatg tcattgagaa 180
tataaagaac agtgccttag aagacagtga aaggtaagct ctagcttaat gtctatgatt 240
t 241

<210> 393
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 393
ggcaggtaca taagcataat cagttatgga cagcttcttg tataaattgc tattcancaa 60

tacataaaact gcctnaaaga tttatgctta caggtagaca ttcaatttac caataaaaca 120
gcatgttctg aaaatatgg cacatttaa aacatattaa gacagtctg ttaaccataa 180
tagtcccaca gtatgactga gtaataagaa tctacttcaa aagnaaaaaa aaaattaatc 240
a 241

<210> 394
<211> 241
<212> DNA
<213> Homo sapiens

<400> 394
aggtagcgcgcactgatg gctgcaacaa ctttcctcct accccagccc agaaaatatt 60
tctccccac cccaggatcc gggaccaaaa taaagagcaa gcaggcccccc ttcaactgagg 120
tgctggtag ggctcagatgc cacattactg tgctttgaga aagaggaagg ggattttttt 180
ggcactttaa aaatagagga gtaagcagga ctggagagggc cagagaagat accaaaattg 240
g 241

<210> 395
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 395
nggcnnnnnc caanatataa aatntnanta tnatacatga taaaaagctt tatntatttt 60
agttagataat taagtttaca ctgtgataaa ggattaattc ccagatgacc atctacagtt 120
actaccacat agagggtata cacggatgga tcgattacaa gaatataaaa cttatttcc 180
ttcctgtatc cacatttctt tgcaatgtga atttgcaggc cctctcaaga agtggagtct 240
a 241

<210> 396
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 396
gaggtacacc ttgaatgaca atgctnggag cccccctgtg gtcatcgacg cctccactgc 60
cattgatgca ccacccaacc tgcgtttcct ggccaccacaa cccaatcct tgctggatc 120
atggcagccg ccacgtgccaa ggattaccgg ctacatcatc aagtatgaga agcctgggtc 180
tcctcccaga gaagtggtcc ctggccccgg ccctgggtgtc acagaggcta ctattactgg 240
c 241

<210> 397
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 397
ggcaggtacc agcaggggga tgtgtttctg gggattgtg gctcttggaa cttcacggtt 60
tcccaatg tggaaaat atctgtgc gatagaaatc ctggccagag gctgtttctg 120
tctcatttga gctcttccttc atgtggcaga gctgactgtg ggggtttagg agccctacatt 180
ttagaaaagc ttacctcaaa gttctgcatt gagccttgagc actggaaaagg agataaaaata 240
a 241

<210> 398
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 398
gangtacca ngacatcacc tnacacntgg aaagcganga nttgaatggt gcuitacaang 60
ccntaccncnt tgcccannac ctgaacgcgc ctntgattt ggacagccgt gggaggaca 120
gttatgaaac nantcanctg gatgaccana gtgntgaaac cnacannac angcnntcna 180
cattatataa ncggaaaagct aatgtgaga gcaatgtca ttccgatgtn attgatagtc 240
a 241

<210> 399
<211> 241
<212> DNA
<213> Homo sapiens

<220>.
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 399
cagagtgaga tgggagtggg agggccaatc tgatacagaa ggggttgaag ggttagggccc 60
ctgagcagcc cacccttac cctgacgaag gcaatcctcc tctggaatgt ctctccctc 120
ttcagtctgg gttctgcctc agccacgaac tgggaaggag tgaggaacat cccaacggca 180
atgagagtat cccagtgact ccaaacagga angaatcagt gttcanaaag tcagggccct 240
t 241

<210> 400
<211> 241
<212> DNA
<213> Homo sapiens

<400> 400
ggtaactcttg ctcttttagc tagagtgtat gtgaaaataa agaaatacat cattgtattc 60
acaaccatgt gtcttcattt ataactttt gttaaaaaaa ttttagttc aagtttagtt 120

cattgatatt atccctctgaa tgca~~gtt~~taag gctggcaga aattctactc atgtgacatc 180
tgccacaggt ctat~~ttt~~gaa gctttcttc taatggcaa t~~gttt~~gcct taccaggatt 240
t 241

<210> 401
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 401
nn~~c~~aggtact ttgttagagca gagagaggct ttgg~~t~~tc~~c~~tc ctttcttcaa tcacgtggag 60
atgtgtcatc acctgggatt t~~c~~atctggc cgc~~c~~tttct ggg~~t~~caacag ccaacacatg 120
ctgt~~a~~atga cg~~g~~atggtat gtaagcgatc tt~~t~~gttctca gcacggacat aacg~~cc~~gtaa 180
ggc~~c~~tggaga atgc~~g~~atgag gccgtggcgg gtcagactgc aaggcagcca ggtagttctc 240
c 241

<210> 402
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 402
ggc~~c~~agg~~t~~cca aaaaaa~~ac~~ct aaaaanngtt tcaggaatgt agagaaat~~at~~ ccaactt~~aa~~ 60
tagc~~g~~aaaaaa gtgc~~c~~ccata attactgctg cactgc~~ag~~tc atttctgcaa ttccc~~at~~gtt 120
tct~~aa~~at~~aa~~ c~~t~~atctt~~g~~tc agataacaca caatataa~~ag~~ agcaattat~~g~~ aaaaacagac 180
att~~t~~acat~~at~~ a~~t~~tct~~aa~~ag t~~c~~ttatt~~gg~~ aat~~t~~atc~~c~~t~~g~~t ttggccatt~~g~~ ggataac~~cc~~aa 240
t 241

<210> 403
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 403
agg~~t~~gtt~~a~~ac t~~ac~~cc~~c~~t~~cc~~ gagac~~gg~~gat tgatgac~~g~~ag tcctatgang ccat~~ttt~~caa 60
g~~cc~~gg~~t~~cat~~g~~ t~~c~~ccaa~~gg~~taa t~~gg~~gagat~~gtt~~ ccag~~c~~ct~~g~~tag~~t~~ g~~cg~~gtgg~~t~~ct tacagtgt~~gg~~ 120
ct~~c~~ta~~g~~act~~cc~~ c~~t~~atct~~gg~~gg atc~~g~~gtt~~agg~~ tt~~g~~ctt~~ca~~at ctaactat~~ca~~ aaggacac~~gc~~ 180
ca~~ag~~tg~~tg~~tg gaattt~~gt~~ca agagct~~tt~~aa cctgc~~c~~tat~~g~~ ctgatgct~~gg~~ gaggc~~gg~~gt~~gg~~ 240
t 241

<210> 404
<211> 241
<212> DNA
<213> Homo sapiens

<400> 404
caggtactgc aacccataaa atactgtttc ctcatatttc accttcctta atttggagtt 60
ttctgtcttc ttttacacgcgca attcaaagta ggaataaaact ttgcttggtgt tgggtggata 120
ttgtttatag tgagtaacct tgttaggagtc ggtggccagg aggatgtga actcggcttc 180
tgcccgacgga ttcatctcg gccggaggac aagggggcccgcga gctccctgac 240
c 241

<210> 405
<211> 266
<212> DNA
<213> Homo sapiens

<400> 405
ttctgggctg gggagtggag agaaagaagt tgcagggctt acaggaaatc ccagagcctg 60
aggttttctc ccagatttga gaactctaga ttctgtcatca ttatcttga gtctatattc 120
tcttgggctg taagaagatg aggaatgtaa taggtctgcc ccaagccctt catgccttct 180
gtaccaagct tggcccttg tgcatcttc ccaggctctg gctgcccctt attggagaat 240
gtgatttcca agacaatcaa tccaca 266

<210> 406
<211> 231
<212> DNA
<213> Homo sapiens

<400> 406
ttggtaaga accattcctc ggcattcttg cggttcttct ctgccccatctt ctcatactgg 60
tcacgcattct cgttcagaat gcggcgtcagg tccacgcccag gtgcagcgtc catctccaca 120
ttgacatctc cacccacctg gcctctcagg gcattcatct cctccctcggtt gttttcttc 180
aggtaggcca gtcctccctt caggctctca atctgcattt ccaggtcagc t 231

<210> 407
<211> 266
<212> DNA
<213> Homo sapiens

<400> 407
cagcatcatt gtttataatc agaaactctg gtccttctgt ctgggtggcac tttagagtctt 60
tttgtccata atgcagcagt atggagggag gatTTTATGG agaaatgggg atagtcttca 120
tgaccacaaa taaataaaagg aaaactaagc tgcattgtgg gtttggaaaa ggttattata 180
cttcttaaca attcttttt tcagggactt ttcttagtgtt atgactgtta cttgaccttc 240
tttggaaaagc attcccaaaa tgctct 266

<210> 408
<211> 261
<212> DNA
<213> Homo sapiens

<400> 408
ctgtgtcagc gagcctcggt acactgattt ccgatcaaaa gaatcatcat ctttaccttg 60
acttttcagg gaattactga actttcttc cagaagatag ggcacagcca ttgccttggc 120

120

cctcaacttcaa ggggtctgcat ttgggtcctc tggtctcttg ccaagttcc cagccactcg 180
aggagagtaat atctggaggg caaagaagag acttatgtta ttgttgaacc tccagccaca 240
gggaggagca tgggcattggg t 261

<210> 409
<211> 266
<212> DNA
<213> Homo sapiens

<400> 409
gctgacagta atacactgcc acatcttcag cctgcaggct gctgatggtg agagtgaat 60
ctgtccccaga cccgctgcc a ctgaatcggt cagggatccc ggattcccggt gtatgtgccc 120
agtaaatgag cagtttagga ggctgtcctg gtttctgctg gtaccaagct aagtagttct 180
tattgttggaa gctgtctaaa acactctggc tggtcttgca gttgatggtg gccctctcgc 240
ccagagacac agccaggagag tgtggaa 266

<210> 410
<211> 181
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 410
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tttnggatg gggacttgc aattttctt aaggggnnnn ttnannnnng aagaaaaccn 120
ngntcccggtt ccagccaaac cngtngctna ctttccaccc tntttccacc tccctcnggt 180
t 181

<210> 411
<211> 261
<212> DNA
<213> Homo sapiens

<400> 411
gcccctgcag tacttggccg atgtggacac ctctgatgag gaaagcatcc gggctcacgt 60
gatggcctcc caccattcca agcggagagg ccgggcgtct tctgagatgc agggtctagg 120
tgctggatgt cgacacggagg ccgtatgtaga ggaggaggcc ctgaggagga agctggagga 180
gctggccagc aacgtcagtg accaggagac ctcgtccgag gaggaggaag ccaaggacga 240
aaaggcagag cccaacaggg a 261

<210> 412
<211> 171
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

<400> 412

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 cagagctgta tctgcaggnt cgtaagcata nagacngtt gaatatcttc cagngatatc 120
 ggctctaact gncagagatg ggtcaacaaa cataatcccg gggacatact g 171

 <210> 413
 <211> 266
 <212> DNA
 <213> Homo sapiens

 <400> 413
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 cattttgtta tttgcattaa aattatttt ggtctctgtt caaatgagtt tggagaatgc 180
 ttgacttgtt ggtctgtgtaa aatgtgrata tataatatacc tgaatacagg aacatcgag 240
 acctatttcac tcccacacac tctgct 266

 <210> 414
 <211> 266
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(241)
 <223> n = A,T,C or G

 <400> 414
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 ggaatccatg tgtttgcaaa aaaagtgtgc tanttttaag gnctttcgta taagaatnaa 180
 tganacaatt ttccttaccaa aggangaaca aaaggataaa tataatacaa aatatatgtt 240
 tatggttgtt tgacaaatta tataac 266

 <210> 415
 <211> 266
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(241)
 <223> n = A,T,C or G

 <400> 415
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 gtttgcgcaaa cgttggcc attgtcacag gcacgtggt gtacgtctcg tcgattggta 120
 tggcttcatt cagctccggc tcccaacgat caaggcgagt tacatgatcc cccatgttgt 180
 gcaaaaaaagc ggttagctcc ttccggccctc cgatcggtgt canaagtaag ttggcccgag 240
 tgttatcact catggttatg gcagca 266

 <210> 416
 <211> 878
 <212> DNA
 <213> Homo sapiens

<400> 416
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tatcacaaaa tgacttgtac acagtagttt acaaacgactc ccaagagagg aaaaaaaaaa 120
aaaaagacgc ctcaaaaattc actcaacttt tgagacagca atggcaatag gcagcagaga 180
agctatgctg caactgaggg cacatatcat tgaagatgtc acaggagttt aagagacagg 240
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aaaagggtctc ctttcaactat tcaggaaggg aagtggaaagg agaaattaac caattccctgc 720
cacagcagcc ctttttggtc gcttccacaa tagatacttt atggaggtgc acagccaacc 780
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<210> 417

<211> 514

<212> DNA

<213> Homo sapiens

<400> 417
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caccagcg gaggtggat gtgagacagc ccacattgga aaatccagaa aaccgggaac 180
aggatttgc ctttcaaat tctactcccc agatcctctc ccctggacac aggagaccca 240
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accagggtcc aggactaagg cgtttctcc atagcctcaa cattttggga atcttccctt 420
aatcacccctt gctctcttg ggtgctgga agatggactg gcagagacct ctttgtgcg 480
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<210> 418

<211> 352

<212> DNA

<213> Homo sapiens

<400> 418
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agtaggctca ggatctgcgt aaggtcggag gagttagtc ccccaatcaa gagcctgtct 180
tcctgaagcc ttgggtgata ttttgcact cagccaaagaa tgaggatgca tccttcagat 240
tctctatgtc ccgaacctgg aaccatcca cggcagctt cagccaaac tccagagcat 300
cttcacctt ggtggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 352

<210> 419

<211> 344

<212> DNA

<213> Homo sapiens

<400> 419
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attgagactc aaaggcttat actggcgtct gaaactatgt cttcgtaa acccgatattt 180

ggctgcaggc ccagttctca tgctgccctt gggtgccat ctgttaacag aggagaacgt 180
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 catcatcatt attaaaacttc agaaaagcag cagccatgtt cagtcaggct catgctgcct 300
 cactgcttaa gtgcctgcag gagccgcctg ccaagctccc cttcctacac ctggcacact 360
 ggggtctgca caaggcttgc tcaacccaaag acagcttccc cttttgatt gcctgttagac 420
 tttggagcca agaaaacactc tggctgactc tacacacact tcaggtggtt tggcttcaa 480
 agtcattgtat gcaacttggaa aggaaacagt ttaatggtgaa atatgaacta ccatttataa 540
 cttctgtttt tttattgaga aaatgattca cgaattccaa atcagattgc caggaagaaa 600
 taggacgtga cggtacttggg ccctgtgatt ctcccagccc ttgcagtcg ctaggtgaga 660
 ggaaaagctc tttacttccg cccctggcag ggacttctgg gttatggagaa aaaccagaga 720
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<210> 423

<211> 1041

<212> DNA

<213> Homo sapiens

<400> 423

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 gccttccag gatgggggtc ttttctgctc ccagcggata gtggaaacccc tgctgcacc 180
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 gcagagtaac gtggaaagtttgg tcccacaccta cccggccacatgtgatc acatgaaccc 420
 cggcaacctg cacctgttca tcaatgccta caacaggat tggatgttag tttagccaca 480
 tcattgttat ttatgagggtg ttttctgttag atccgaaatgt tgggacagat gagagggaga 540
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 gtccccagga aggacacccgt gcctgtaaagc tgggtcctgg cattcagctc gcctgcagg 660
 gatctgaaca aacactccag accactgggg gtgcagacgt gagagggacg cagtcgcaca 720
 ctcagagggt tgagagtaaa tatgtgtgcc cgctgtgac ctccacgaaa ggc当地atgt 780
 aagaagagct aagtggagaga gcagcaaaagc actccctggag gccggggata atccaggcag 840
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 cgtggccctc tcaaccagca ctaggtgctt atctggagct cagctagggg aggagacagc 960
 tcagggccat tgggtgtcgc cagagactct gtaatcttcc agggagctcg ctcaacctgc 1020
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<210> 424

<211> 1288

<212> DNA

<213> Homo sapiens

<400> 424

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 ggacccaaagc gaaaaaggta tctcaagact aacggccgga atctggaggc ccatgaccca 180
 gaacccagga aggatagaag cttgaagacc tggggaaatcc ccaagatgag aaccctaaac 240
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 tcttaagcc tgattttttt gagatgtact ttttgcgtatc gcccgttacc ttttagattga 360
 cagattatgt cctggccag ttttgcgtatc gttttaaatcc acagtttttta cctattttt 420
 aggtatagt gttttgtaaa ctttgcgtatc tattcacatc ttctccactt gagagagaca 480
 caaaaatcca gtcagttatct aatctggctt ttgttaactt ccctcaggag cagacattca 540
 tatagggtat actgtatttc agtcccttct tttgacccca gaagccctag actgagaaga 600
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 agatgtccca ggccaaatgag aagaatttgcgaaatc acagatgtgc cagacttctg 720

agaaggcacct	gccagcaaca	gcttccttct	ttgagcttag	tccatccctc	ataaaaaatg	780
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aaggaattaa	gtggcttcgt	cattgtcc	ctacctcaaa	gataatttat	tccaaaagct	1080
aagataaatg	gaagacttct	gaacttgtga	actgtatgtga	aatgcagaat	ctctttttag	1140
tctttgtgt	ttggaaagatt	gaaaaatatt	gttcagcatg	ggtgaccacc	agaaaagtaat	1200
cttaagccat	ctagatgtca	caattgaaac	aaactgggaa	gttggttgct	attgtaaaat	1260
aaaatatact	qtttqaaaa	aaaaaaaaac				1288

<210> 425
<211> 446
<212> DNA
<213> *Homo sapiens*

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<400> 425
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gcctaacatc ttccacaagg atccccatgt gaacatgctg cacgtgtttg ttctggcg 120
atggcagccc atcgagtagc gcaagaagaa gctgaaaatac ctggccctaca atcaccagca 180
cgaataacttc ttccatgtatttgc ggcggccgc gctcatcccc atgtatttcc agtaccagat 240
catcatgacc atgatcgtcc ataagaactg ggtggacactg gcctggggccg tcagctacta 300
catccgggttc ttccatcacct acatcccttt ctacggcata ctgggagcccc tccttttcct 360
caacttcatac aggttcctgg agagccactg gtttgggtgg gtcacacacaga tgaatcacat 420
cgtcatggag attgaccagg aggacc 446
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<210> 426
<211> 874
<212> DNA
<213> *Homo sapiens*

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<400> 426
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acattctaca atggaaactt ttatataatg ctgcattgtac tgtgctatgg accacgcaca 120
tacagccatg ctgtttcaga agacttgaaa tgccattgtat agttaaaaaa ctctacacccc 180
gatggagaat cgaggaagac aatthaatgt ttcatctgaa tccagagggtg catcaaatta 240
aatgacagct ccacctggca aataatagct gttacttgat ggtatccaag aagaaatgg 300
tggtgatgga taaattcaga aatgtttccc caaagggtggg tggttttaa aaagtttca 360
ggtcacaacc cttgcagaaa acactgtatgc ccaacacact gattcgcggt ccaggaaaca 420
cggttcttcc aagtccaaag gggctgggggt tccccaaacgta tcaagttccct gtgctgtat 480
caagagggtc ctttgactg gatagggagc acttgggagc tgtacaccat cagtcataat 540
ggatggcagt gtaaaagatg atccaaatgat cctgagatgc tcctgaggag tggtgaccca 600
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tccagagcag caatggccctt tcctgttaaca ggaaaaaaaaagc ctctgttat tcccaagaac 720
cctcgttaatg gcaaaactcc ccaaatgaca cccaggacca cagcaatgtat ctgtcgaaac 780
cagtagatca catttaaaaa ttcatccctt tcctccagg ccgcgtcgct ccgcagcacc 840
ttactccaga cggagacttt gagggccccg ttgg 874

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<210> 427
<211> 638
<212> DNA
<213> *Homo sapiens*

<400> 427

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 ttgatttttc ttcttggaaag agtaaggaaa acctgttaca ttttcaagtt aattcatgtta 120
 aaaaatgata gtgattttga tgtaattttat ctcttggttg aatctgtcat tcaaaggcca 180
 ataatttaag ttgcatacg ctgatattag tagcttgca accctgtatag agtaaataaa 240
 ttttatggcc ggggcacaaa tactgtgtg aatcttattt tatagtatcc atgaatgaat 300
 ttatggaaat agatatttgc gcaat ttatgcagag attaaatgac atcataatac 360
 tggatgaaaaa cttgcataga attctgatta aatagtgggt ctgttcacca tgtgcagtt 420
 gaagtattta aataaccact ctttcacag tttatatttct tctcaagcgt tttcaagatc 480
 tagcatgtgg attttaaaag atttgcctc attaacaaga ataacattta aaggagattt 540
 tttcaaaaata ttttgcaaa ttgagataag gacagaaaaga ttgagaaaaca ttgtatattt 600
 tgcaaaaaca agatgttgc agctgttca gagagagt 638

<210> 428

<211> 535

<212> DNA

<213> Homo sapiens

<400> 428

acaagatgtat tttccctcct caatttgaca gatcaaagaa gatatcccttgc ttaattcaag 60
 tgtatggtgg tccctgcagt cagagtgtaa ggtctgtatt tgctgttaat tggatatctt 120
 atcttgcaag taaggaaggg atgtcatttgc ctttgggttggaa tggtcgagga acagctttcc 180
 aagggtgacaa actcccttat gcagtgtatc gaaagctggg tgtttatgaa gttgaagacc 240
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 ttttcaaatg tggatagca gtggctccag tctccagctg ggaatattac gctgtctgtct 420
 acacagagag attcatgggt ctcccaacaa aggatgataa tcttgcac tataagaatt 480
 caactgtgtat ggcaagagca gaatatttca gaaatgtaga ctatcttctc atcca 535

<210> 429

<211> 675

<212> DNA

<213> Homo sapiens

<400> 429

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 ttagatcgaa gcacaagcac aagccactga tattctctat gtgatcagggt ttttacaaaaa 120
 aaatacatag ttttcaataaa ataatgttta attttacaaac tttgatcatacg caatgtcata 180
 caccgtttca acacactaca ctctgcatac tagatagtct acgagaagac gaaactttgc 240
 catgcatttt ctttcccccc tagtgcatac aaacacttca tcctccagcg cactgcctca 300
 ggtagcttta ctttctcttct gtttccacagc aataggccgt gctgtggcat gcaaacttcta 360
 aaaaagggtcc cccccacaaa ccactcagac ttctacacaa aagggttttt cagctttct 420
 gctcccaaac ctggagttggc taagaaaatg agtttcatgt ggccttggaa aatacacact 480
 tggatcacttgc ttttccatgc ttttccatgc ttttccatgc ttttccatgc ttttccatgc 540
 gtcacgaagc attatgggt gccataacca cttaggatcc caaaccggaa aaaaataggcc 600
 tccgttttaa aacagtcaat tcaaaaaagg tggatcacttgc ttttccatgc ttttccatgc 660
 acccacaaca tatgt 675

<210> 430

<211> 434

<212> DNA

<213> Homo sapiens

<400> 430

acctctgcca gaagtccagc gagaggacct cacagtagag cacaggccac tccgggagtg 60
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gagccacctt gtccattgcc agggacttgg tgggtgcagg ctgtgttact cctgagagct 180
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 cacctgggac agtcatctca aagtccgtgc ctacgaggct gctgagatac tccttgc 360
 ggcataaaag atccttgaac actcgccgtt cccgccttc ctccctccgc tggcgtggg 420
 gggaaacatt gtcg 434

<210> 431
 <211> 581
 <212> DNA
 <213> Homo sapiens

<400> 431
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 caagtgcacca agaccagaag caggacgt taggcttagtt ctgcggcaag gtgaactgga 180
 gaccctgtct ctgccttc tccctggcct gtcccacaga catcccggtt ttaaccac 240
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 caagcaccac tggatggctc tggagccagg ggacttctat gcacatacaa ccaacatcac 540
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<210> 432
 <211> 532
 <212> DNA
 <213> Homo sapiens

<400> 432
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 cttgacagtc atgtgtttt taagtcttgc attaccatg actacattct tagccaggtg 180
 ctgcataact ggaagaagag attcttcagt atatgacagg taatgttgc gagttgggtgt 240
 ccattccacca ttatccagaa ttttcgtgc taagcaaaaa gtcctgtgc caatttgaga 300
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 tagaggccga cccagaccaa agtttaaagc tctttagatc ttcatatcca tctgtctgtat 480
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<210> 433
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 433
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 acactacagt ggttttagaaa ttacttaattt tacttctaaag tcattctaaa accttgc 120
 tggaaatgact tcttaatattt ttagttgtata gactgttaca ggttaataggg acttagcaag 180
 ctctttata tgcataagga gcatcttatca gattaaggta gaacatttgc tgcagccac 240
 atattttagat gacacttaggt gcaatagcag ggatagattt tgggtgttgc tagtctcatg 300
 ccttgagatc tgggtgttgc ttcaaatgg tggccagcca gatcaaggat gtagtatctc 360
 atagttccca ggtgatattt ttcttatttag aaaaatatta taactcattt gttgtttgac 420
 actttagat tggaaatccc taatttatttc taaaattttaa gttgttctttt ggttccagtg 480
 ctttatgttg ttgttgc tggatgggtt tacatattat atgttctaga a 531

<210> 434
<211> 530
<212> DNA
<213> Homo sapiens

<400> 434
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agaaggatgc ctagcttat cagtgaagga acttccaaca gtcaccacta atgtgcagaa 120
ctctcaagat aaaagcattg aaaacatgg cagtagtaaa atagaaacaa tgaataagtc 180
tcctcatatc tctaatggca gtgttagccag tgattattt gatttgata agattactgt 240
gaaagatgat gttgggtgtt tcaggaa aagaaaagca gcatctaaag ctgcagcaca 300
gcagaggaag attcttctgg aaggcagtga tggtgatagt gctaatgaca ctgaaccaga 360
ctttgcacct ggtgaagatt ctgaggatga ttctgattt tggagatgtt aggataatga 420
cgaaagacttc tctatgagaa aaagtaaagt taaagaaatt aaaaagaaag aagtgaaggt 480
aaaatccccca gtagaaaaga aagagaagaa atctaaatcc aaatgtatg 530

<210> 435
<211> 677
<212> DNA
<213> Homo sapiens

<400> 435
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tccaaaatca tttataaaat gtatttgct ttggaaatcca caggacttca aacaagcaaa 180
gtttcactgc agatagtcac aaagatgcag atacactgaa atacttaaga gccttattaa 240
tgatTTTGT tattttggat cttctgtttt tttcttattaa tggtccgaag cttctttaat 300
accaatttat cagacagaag catgtcatct tttttttcaa gataatccag taaattttca 360
gtccattcaa gtgccgcctt atggctaata cgcttctctg gattcagttc tttttttcta 420
ctcttactgg aaggcttttgc ttcagcagcc ttggctgtt cctcagcact ttcaactgtca 480
gtcagcacct gacagcttgc gtcactgctc cgagagtcga accactgatc aatattctca 540
atgtcaacat gttcacatc ttctgtgttc tggtaaaactg ttgtttaattt agctgctaaa 600
atggctcctt catcaatgtt catacctgaa ttctcttcat tgccaggaa aagtttttca 660
catgtttgg ttatgg 677

<210> 436
<211> 573
<212> DNA
<213> Homo sapiens

<400> 436
acctcttagg gtgggagaaa tggtgaagag ttgttccctac aacttgctaa cctagtggac 60
aggtagtag attagcatca tccggataga tggtaagagg acggctgttt ggataataat 120
taaggataaa atttggccag ttgacagatt ctgtttccag cagttttac agcaacagt 180
gagtgcattca gtattgtttt cctgttaattt taattttgcat ccgcaatcat ttggatataca 240
atgctgtttt aagttttgtc ctattggaa agtcttgcgt tgcagggtt cagtttaagat 300
cttgcgtatg aggaatggaa tgggcttaattt ttttgcgtt ttcttgcatt tggtttttcat 360
gcaaaatacag taggtagtt tagtcttta cacagaacat gataaaactac acctgttgc 420
gtcaccgtct gtcaatgaat attatagaag gtatgaaggt gtaattacca taataacaaa 480
acaccctgtc tttagggctg accttcgtc ctttgacctc ctcagccctcc attccatct 540
tcgctcagac tgcaagtatg ttgttattaa tgt 573

<210> 437
<211> 645

<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(645)
<223> n = A,T,C or G

<400> 437
acaattggta tccatatatctt gttgaaattg taatgggaaa acaatatatt tcaatctcta 60
tgttagatgt gggttttgt tttcataata tattcttttta gtttactgta tgagtttgc 120
aggactgcat aatagatcac cacaatcata acatcttagg accacagaca ttatgagat 180
catggcttcgt gtgggttaga agtatgctca tgtcttaact gggtcctctg ctcagtctta 240
tctggctgca atcaaggtgt cagctggct gaattttcat ttggaatctt gactgggaaa 300
gagtctgctt ccaaggtcat gaagtttgct gcacaaatgt atgttttat gacagtatga 360
ctgaaatccc aagctatctc ctgactttta gctggtaat ctcaggccct aaatgttgcc 420
tacagttcct agaggctgtt cacagttctt agccatgtgg atttcctcaa catggctgct 480
tgcttcatca agtcagcaag aatagcctgt catatcagtg tatatcaggc tcactcagga 540
taatttccct actgatgagc caaacactaa ctgatTTAG agcttaacta catctgcaaa 600
attcngrtca ccagaggca gtcatttca ggaaaggaga agtgt 645

<210> 438
<211> 485
<212> DNA
<213> Homo sapiens

<400> 438
acagaattga gagacaagat tgcttgtaat ggagatgctt ctagctctca gataatacat 60
atttctgatg aaaatgaagg aaaagaaaatg tgtgttctgc gaatgactcg agcttagacgt 120
tcccaggttag aacagcagca gctcatcaact gttgaaaagg ctttggcaat tctttctcag 180
cctacaccct cacttggat ggatcatgag cgataaaaaa atctttgaa gactgttgg 240
aaaaaaaaatgc aaaaactacaa catatccatg ttggaaaatt tttatgtcgtt aatcagccaa 300
tgtatTTATC ggcatcgcaaa ggaccatgat aaaacatcac ttattcagaa aatggagcaa 360
gagtagaaaa acttcagggtt ttccagatga tgatgtcatg gtatcgatgat ttctttat 420
tcagttccta ttttaagtcat ttttgcatttgc tccgcctaat tgatgttagta tgaaaccctg 480
catctt 485

<210> 439
<211> 533
<212> DNA
<213> Homo sapiens

<400> 439
acagcagttt cctcatccct gcagctgtgt ttgaacaggt catttaccat actgtccctcc 60
aggttcaaca gtatggctcc aatgtatgaa atttcattctt gatTTTCTGG ctgaagacta 120
ttctgtttgt gtatgtccac cacagttact ttatcccttc atctgtggat gggcagaatg 180
aaacatataat gggaaatgttc tgtcaataa aaacagcagt ggtAACACAG atgttaggctc 240
tgagtgtctc actggagact gaagttccaca gatatgcaac aaaggcccttgc tctccctgat 300
gtttttgcct cctgctggtc atgtgttttc acacatcaag agaggacatt taacatttga 360
gccacagtgt catttgcgtt tgtctgtatgg ttgggtggca gagaatttga actggagatg 420
aacatttatta tccaggacgc tgagagtata acatgcatga cagagctttt agagcactgt 480
gatgtacat gtcaaggcaga aatagggagc atgtttacag ccatttcatg aaa 533

<210> 440
<211> 341

<212> DNA

<213> Homo sapiens

<400> 440

catgggttag ggggtcggg gattcattga atttgttttg gcaggagcaa gccctgtca 60
cactctcaca ctcgcaccca gaattgtcaa agatacagat tgtaaaaatc tacatccct 120
cagtctcaact cacaaaaaat aaaatctcat gtcccaacg aacccagagt cagacgacag 180
ctggaggcatt ggcagggaca gtcagaaagg agacaagtga aaacggtcag atggacacag 240
gcccggggaga aaagacagag ggagagagac catcgaaac aatcagaggg gccgagacga 300
tcagaaaagg gtcagcccgaa gacaggctga gccagagttt c 341

<210> 441

<211> 572

- <212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(572)

<223> n = A,T,C or G

<400> 441

aatgtttttttt atgcagcaag agataataca caggacttct canagcactt 60
aatatgttaa tataaatctc caaaaaaaaaa gatatacaat gaaacattcc tcttagttat 120
ctggccaagg anactttttt ttttganaaa tatttttcaa aaagctgatc taatgatatg 180
gctctggtcc tacaatttca tgtaacttct aacccttgatt ttatctcatg agcaaatcat 240
ttatccttcc agaacctcaa ctttccctt ttacaaaaga gaaataaaacc atctgccttt 300
acataaaatca ttaatacagc cctggatggg cagattctga gctatttttgc gctgggggg 360
ggaaatagc ctgtggaggt cctaaaaaga tctacggggc tcgagatggg tctctgcaag 420
gtacgaggtg ggctcagggc ccatttcagt ctttggccc caggccattt ccacaaaatg 480
gtgagaaaata gtgtcttctt ttagcttgcataactcaa agatgggggg catggacctg 540
ggcccttctta ggcttagggca tgaaccttcc cc 572

<210> 442

<211> 379

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(379)

<223> n = A,T,C or G

<400> 442

tcccaagctgc actgcttaca cgtttccctt cgtnntcacc taccccgagg ctgactcctt 60
cccccaagtgt gcagctgccc accgcaggg cagcagcagc aatgagcctt cctctgactc 120
gctcagctca cccacgctgc tggccctgtg agggggcagg gaaggggagg cagccggcac 180
ccacaagtgc cactgcccga gctggtgcatt tacagagagg agaaacacat cttccctaga 240
gggttctgt agacctaggg aggaccttat ctgtgcgtga aacacaccag gctgtggcc 300
tcaaggactt gaaagcatcc atgtgtggac tcaagtcctt acctcttccg gagatgtac 360
aaaacgcattt gagtgtgt 379

<210> 443

<211> 511

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(511)

<223> n = A,T,C or G

<400> 443

acatgccccaaaggctcgc ttcattgcta cgattctcta cttaaatcca cattcacagc 60
tattgcctca gaccctctgg aggaggggcc aggggttagc tggcttgaa tagcatgtag 120
agcacaggca gtgtggccac aaatgtcaca caggtgacca gggtgtata gatgggttgc 180
ctgttgcatt gggcttctag tctctgtcc gtgtctgaca gtgccaagat catgtcccc 240
tgctccagca agaagctggg catagccccg tctgtcggtt ccaccaggcc tgggtgtgct 300
gcagacttta caagctgaac caccctagcc atttggctac aagtctttc taggccatca 360
agctgctctc gtaagccttc tagacatgaa tggacttgcc tggaatgact aagctgctct 420
ttcaaggcag ctgaaaaggac atcnacatct ctgtctctgg tcgggggact acctgcctgt 480
gaccagact cctgcccctgg cccagcagca t 511

<210> 444

<211> 612

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(612)

<223> n = A,T,C or G

<400> 444

acaggaagaa ttctacagtt aatctatcac agtgttccag caaagcatat gttaaaaact 60
acagtttca atctaacatc taaattttaa aaagtagcat ttcagcaaca aacaagctca 120
gagaggctca tggcaaaagt gaaataacag aactattgct cagatgtctg caaagtcaag 180
ctgtgcct cagctccgccc cacttgaagg cttaggcaga cacgttaagg ggcgggtggct 240
ccttggcagc accattcaca gtggcatcat catacgagg tagcagcacc gtatgtcat 300
tgctggtaac ataaaccagg acatcagagg agttcctacc attgtatgtat cggtagcagt 360
tccaaacaca gctaatcaag taacccttaa aagtcaagat aatgctaata aacagaagaa 420
taataaggac caaacaggtt ggatttactg acatgacatc atctctgtat ggaaaaattag 480
gaggcagttt ccgtatgtat tcctgaatgg agtttggata aataagcaca gtgattgcaa 540
ccaacanctt cagggcaaag tcaaagatct ggtaacagaa gaatggatg atccaggctg 600
cgcgttgctt gt 612

<210> 445

<211> 708

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(708)

<223> n = A,T,C or G

<400> 445

accatcctgt tccaacagag ccattgccta ttcctaaatt gaatctgact ggggtgtgcc 60
ctcctcgaa cacaacagta gacctaata gtggaaacat cgatgtgcct cccaaacatga 120
caagctggc cagcttcat aatggtgtgg ctgctggct gaagatact cctgcctccc 180

agatcgactc agcttggatt gtttacaata agcccaagca tgctgagttg gccaatgagt 240
atgcgtggctt tctcatggct ctgggttga atgggcacct taccaagctg gcgactctca 300
atatccatga ctacttgacc aagggccatg aaatgacaag cattgactg ctacttggtg 360
tttctgtgc aaaacttaggc accatggata tgtcttattac tcggcttgtt agcattcgca 420
ttctctgtctt cttacccca acgtcccacag agttggatgt tcctcacaat gtccaagtgg 480
ctgcagtggc tggcattggc cttgtatattc aagggcacgc tcacagacat actgcagaag 540
tcctgttggc tgagatagga cggcctcctg tccttgaaat ggaatactgc actgacagag 600
agtcatactc cttagctgct ggcttggccc tgggcatggt ctnttgggg catggcagca 660
atttgatagg tatgtntgat ctcaatgtgc ctgaggcagct ctatcagt 708

<210> 446

<211> 612

<212> DNA

<213> Homo sapiens

<400> 446

acaagcaacg cgcagccctgg atcatccat tcttctgtta ccagatctt gactttgcc 60
tgaacatgtt ggttgcatac actgtgctt tttatccaaa ctccattcag gaatacatac 120
ggcaactgcc tcctaatttt ccctacagag atgatgtcat gtcagtgaat cctacctgtt 180
tggtccttat tattcttctg tttatttagca ttatcttgac ttttaagggt tacttgatta 240
gctgtgtttg gaactgctac cgatacatca atggtaggaa ctccctctgat gtcctggttt 300
atgttaccag caatgacact acgggtctgc taccggcgtt tgatgatgcc actgtgaatg 360
gtgctgccaa ggagccacccg ccacccctacg tgcctgccta agccttcaag tgggcggagc 420
tgaggccagc agcttgcatt tgcagacatc tgagcaatag ttctgttatt tcactttgc 480
catgagccctc tctgagctt tttttgtctg aaatgctact ttttaaaatt tagatgttag 540
attgaaaact gtagtttca acatatgctt tgcttggaaaca ctgtgataga ttaactgttag 600
aattcttcct gt 612

<210> 447

<211> 642

<212> DNA

<213> Homo sapiens

<400> 447

actgaaaagaa ttaaaagtccat aagtcttccc aaaacaaaaaa gaactgccc cagagaaaat 60
cctttctgtat acttttcatt gctaaaataa aacaggcggg aaatgtggaa aagaaattca 120
acaaaataat gtagcaccag aagaacaagt cctagatgat tcaaggtaaa aaggttaagct 180
ccagcaatgt ggaagaggtt aagaccaatg tagacaagct gacgaggaat atcttctttt 240
ttgggtttctt ggaagttagag ttccaggaaaa gcatgaagcc agtaagccag ctgtgatatg 300
tagaaaaactt tcattttgaaa tgtcatcagg ttatggggat aagccctcca taagatagtt 360
gggtctgaga tttttttttc agagatgaga atgaatgtgc cccaaacaca ggcaaaaagg 420
tagaacgcac taagctgacc agattcatta aacttgcgtt gttttttttt ggagaagtgc 480
atccgcctgt taattttatc caacatatac tcttgaattt cggcatgaat aattatcgcc 540
actagcatgt agaagaaaaac agtagccaaa tctttgtatgc catagtaata aagggacact 600
gattcagtag ctgtttcttc tttttgtggg agggtagat tg 642

<210> 448

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(394)

<223> n = A,T,C or G

<400> 448
accagaagac cttagaaaaaa ggaggaaagg aggagaggca gataatttg atgaattcct 60
caaagngttt gaaaatccag aggttcctag agaggaccag caacagcagc atcagcagcg 120
tgatgtttatc gatgagccca ttattgaaga gccaaagccgc ctccaggagt cagtgatgga 180
ggccagcaga acaaacatag atgagtcagc tatgcctcca ccaccaccc agggagttaa 240
gcgaaaagct ggacaaaattt acccagagcc tgtgatgcct cctcagcagg tagagcagat 300
ggaaaatacca cctgttagagc ttccccaga agaacctcca aatatctgtc agctaataacc 360
agagtttagaa cttctgccag aaaaagagaa ggag 394

<210> 449
<211> 494
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(494)
<223> n = A,T,C or G

<400> 449
acaaaaaaaca caaggaatac aacccaatag aaaatagtcc tggaaatgtg gtcagaagca 60
aaggcntgag tgcctttctc aaccgtgcaa aagccgtgtt cttcccccga aaccaggaaa 120
aggatccgct actcaaaaac caagaattta aaggagttt ttaaatttcg accttgcattc 180
tgaagctcac ttttcagtcg cattgatgtg agatgtgctg gagtggttat taaccttttt 240
ttccctaaaga ttattgttaa atagatattt tggtttgggg aagttgaattt tttttaggt 300
taaatgtcat ttttagagatg gggagaggga ttatactgca ggcagcttca gccatgttgt 360
gaaactgata aaagcaacctt agcaaggctt cttttcatta ttttttatgt ttcaacttata 420
aagtctttagg taacttagtag gatagaaaca ctgtgtcccg agagtaagga gagaagctac 480
tattgatttag agcc 494

<210> 450
<211> 547
<212> DNA
<213> Homo sapiens

<400> 450
actttgggct ccagacttca ctgtccttag gcattgaaac catcacctgg tttgcattct 60
tcatgactga ggttaactta aaacaaaaat ggttagaaag ctttcctatg cttcgggtaa 120
gagacaattt tgctttgtt gaatttgggg ctgagaaagg cagacagggc ctgattaaag 180
aagacatttgc tcaccactag ccaccaagt aagtgttggg acccaaaggat gacggccatg 240
gaaacgtaga tcatcagetc tgctaagtag ttaggggaag aaacatattt aaaccagtct 300
ccaaatggga tcctgtgggtt acagtgaatg gccactcctg cttttttttt cctgagattg 360
ccgagaataa catggcacctt atactgttgg gcagatgacc agatgaacat catcatccca 420
agaatatggg accaccgtgc ttgcataat agattttcc ctgttatgtt ggcattcctg 480
ccatccatttgc gcaacttggct cagcacagttt aggccaaacaa ggacataata gacaagtcca 540
aaacagt 547

<210> 451
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(384)
<223> n = A,T,C or G

<400> 451
actactnnnt ggttaaaang ccactggtag agtcatctga ntgtaaacaa tgccttgca 60
ctgctggaaa aatccactgg ctcccaagaa aagaaaaatgg tctgaaggct ctgttgtggc 120
tctcacaact catctttccc taagtcatca agtccacat cactgaggc aatgtcatcc 180
tccacggaa gctcgccatc cctgccgtcc caaggctctc tctcaacgat ggtagggaaa 240
gcggccctc ctacagggtgc cggtggagcca cgcccaaag agagctccct gagaaaactcg 300
ttgatgcctt gctcactgaa ggagcctttt agcagagcaa atttcatctt gcgtgcattg 360
atggcggcca tggcgggta cccaa 384

<210> 452
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(381)
<223> n = A,T,C or G

<400> 452
actctaaagt tgccactctc acaggggtca gtgataaccca ctgaacctgg caggaacagt 60
cctgcagcca gaatctgcaa gcagcgccctg tatgcaacgt ttagggccaa aggctgtctg 120
gtggggttgt tcacacagc ataatggcct agtaggtcaa ggatccaggg tggagggc 180
tcaaagccag gaaaacgaat cctcaagtcc ttcaatgtc ttatgagaac tttaactgtg 240
gactgagaag cattttcttc gaaccagcgg gcatgtcggg tggctctaa ncactctgc 300
aatacttta tatccaaatg gagttctgaa tccagtttc naagattggg tggactgtt 360
gtaatganaa tcttcactgt a 381

<210> 453
<211> 455
<212> DNA
<213> Homo sapiens

<400> 453
actgtgctaa acagcctata gccaaatttt aaagagttac aggaacaact gctacacatt 60
caaagaacacag gcattcactg cagccctctg atttgacctg atggggaggga caggagaatg 120
agtcaactctg ccaccacttt tcctgcctt gattttaga ggatttttt tgctctaatt 180
tgtttttctt atatctgccc tactaaggta cacagtctgg gcactttgaa aatgttaaag 240
ttttttaacgt ttgactgaca gaagcagcac ttaaaggctt catgaatcta ttttccaaaa 300
aaagtatgtt ttcagtaaaa cattttacca ttttatctaa ctatgcactg acatttttgt 360
tctccctgaa aaggggattt atgctaacac tgtatttta atgtaaaaat atacgtgttag 420
agatatttttta acttcctgag tgacttatac ctcaa 455

<210> 454
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 454
acagagcanc tttacaagtt gtcacatccc tttataaaatt tttttaaaggc tacagtttaa 60
tacaaaatga attgcgggtt tattacatta ataacccttc acctcagggt tttatgaaga 120
ggaaaagggtt ttatgcaaaa gaaagtgccta caattcccaa tcattttaga cacttttagga 180
gggggtgaag ttgtatgata aagcagatat ttaattatt tgttatcttt ttgtattgca 240
agaaaatttct tgcttagtcaa tcaagaaaaac atccagattg acagtctaaa atggctactg 300
gtatTTTtagt taattcaaaa atgaaacttt tcagtgattc actttactaa cattctattt 360
gagaaggctt attggtaaag ttt 383

<210> 455
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(383)
<223> n = A,T,C or G

<400> 455
actccctttan gacaaggaaa caggtatcatg catgatggta gcagaaaacct tatcaccaag 60
gtgcaggagc tgacttcttc caaagagttg tggttccggg cagcggtcat tgccgtgcc 120
attgctggag ggctgatttt agtggatgtt attatgttgg ccctgaggat gcttcgaagt 180
gaaaataaga ggctgcagga tcagcggcaa cagatgctct cccggttgca ctacagcttt 240
cacggacacc attccaaaaa gggcagggtt gcaaagtttag acttggaaatg catggtgccg 300
gtcagtgggc acgagaactg ctgtctgacc tgtgataaaa tgagacaagc agacctcagc 360
aacgataaga tcctctcgct tgt 383

<210> 456
<211> 543
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(543)
<223> n = A,T,C or G

<400> 456
acaacacatt tacaaaaaag aacattacca atatcagtgg cagtaaggc aagctgaaga 60
atangtagac tgagttccg ggcaatgtct gtcctcaaag acatccaaac tgcgttcagg 120
cagctgaaac aggcttctt cccagtgaca agcatatgtg gtcagtaata caaaacgatgg 180
taaatgaggc tactacatag gcccagttaa caaaactcctc ttctcctcgg gttaggccccatg 240
atacaagtgg aactcatcaa ataattaaaa cccaaggcga taacaacact atttccccatc 300
taaactcatt taagccttca caatgtcgca atggattcag ttacttgcaaa acgateccccgg 360
gttgtcatac agatacttgt ttttacaca taacgctgtg ccatcccttc cttaactgccc 420
ccagtcaggt ttccctgttgt tggaccgaaa ggggatacat ttttagaaatg ctccccctcaa 480
gacagaagtg agaaagaaaag gagaccctga ggccaggatc tattaaacct ggtgtgtgcg 540
caa 543

<210> 457
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(544)
<223> n = A,T,C or G

<400> 457
actgggtccca atattgnat ggtgagctcc tctctaattgt cttccaggc accaatatct 60
gcccatgtca cattaggac agtgcacaaag cttcccttt tggcagaggg ttggactgag 120
gatagagcaa caatgaaatc attcagttca atgcacagtc cttgcattctg ctccctctgag 180
aggggatctt ggtctcttag caaccccagc agcctttgtt attcatcctg ttttcagaa 240
gtgggctcag ttcccagcct ttcctcctgg actccttttag atggcaaatc ttccatttca 300
ggattttct tctgctgttc ctgttagttc attaagactc tattgactgc acacattgt 360
gcctctcgcc acagtgcatt gagatcagca ccaacaaagc ctggagtttag gtgtgctaag 420
tgacagaaaat caaaagcttgg aggaaggcctc agttttctgc acaatgttg aagtattttt 480
tccctggatg cttcatctgg gataacctagg cataatttctc ggtcgaacct tccgcacgt 540
ctca 544

<210> 458
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(382)
<223> n = A,T,C or G

<400> 458
acctntaggc tcaacggcag aancttcacc acaaaaagcga aatggcaca ccacagggag 60
aaaactggtt gtcctggatg tttggaaaat tggtcgttgtt catgggtgt tacttcatcc 120
tatcttatcat taactccatg gcacaaagtt atgccaaacg aatccagcag cggttgaact 180
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<211> 168
<212> DNA
<213> Homo sapiens

<400> 459
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<210> 460
<211> 190
<212> DNA
<213> Homo sapiens

<220>
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<223> n = A,T,C or G

<400> 460

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acctggcgtc accagtggcc cgtctgcctc aggaactcct ccgagtgagg gaggaggggg 180
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<210> 461

<211> 495

<212> DNA

<213> Homo sapiens

<400> 461

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<210> 462

<211> 493

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(493)

<223> n = A,T,C or G

<400> 462

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gtgtaaaagct tgaggctgaa aagtagctt ccagcttcat ttctttgggt tcttgggttag 420
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<210> 463

<211> 3681

<212> DNA

<213> Homo sapiens

<400> 463

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caccctgtgg taattaacct ggtcatcccc accctggaga gccatcctgc ccatgggtga 180
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gaacacctga cacggctgaa agcttggtgg aaaaaacacc tgatgaggct gcacatcctgg 360
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taccaatAGT ctgtgtcaAC agaataCTTA ttttagAAGA AAAATTCTAG atttcttCCT 3540

gaagcctaca gacataaaat aacagtgtga agaattactt gttcacgaat tgcataaaagc 3600
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<211> 1424

<212> DNA

<213> Homo sapiens

<400> 464

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 cacccgtggg taatttaacctt ggtcatcccc accctggaga gccatcctgc ccatgggtga 180
 tcaaagaagg aacatctgca ggaacacctg atgaggctgc acccttggcg gaaagaacac 240
 ctgacacacgc tgaaagcttg gtggaaaaaaa cacctgatga ggctgcaccc ttggtgaaaa 300
 gaacacctgaa cacggctgaa agcttggtgg aaaaaacacc ttagtgggct gcaccccttgg 360
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 agtcagcaga agaaaacacctt agggaaaatta cgagtcctgc aaaagaaaaca tctgagaaat 480
 ttacgtggcc agcaaaaagga agaccttagga agatcgcattt ggagaaaaaaa gaagacacac 540
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 gaagaccttag gaagatcgca tgggagaaaa aaaaaacacc tggtaaagactt ggatgcgtgg 660
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<210> 465

<211> 674

<212> DNA

<213> Homo sapiens

<400> 465

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 cacaccgtg ggtatataac ctggcatcc ccaccctggaa gagccatcct gcccattgg 180
 gatcaaaagaa ggaacatctg caggaacacc ttagtgggctt gcacccttgg cgaaaagaac 240
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 acagtcagca gaagaaacac ctagggaaat tacgagtcctt gcaaaaagaaaa catctgatgaa 480
 atttacgtgg ccagcaaaag gaagaccttag gaagatcgca tgggagaaaa aagatgactc 540
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<210> 466

<211> 1729
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (11)
<223> n=A,T,C or G
<221> unsure
<222> (1128)
<223> n=A,T,C or G

<400> 466

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aagaagacac acctaggaa attatgagtc ccgcaaaaga aacatctgag aaatttacgt 180
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<210> 467

<211> 1337

<212> DNA

<213> Homo sapiens

<400> 467

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<210> 468

<211> 2307

<212> DNA

<213> Homo sapiens

<400> 468

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<210> 469

<211> 650

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (310)

<223> Xaa = Any Amino Acid<221> unsure

<222> (429)

<223> Xaa = Any Amino Acid<231> unsure

<222> (522)

<223> Xaa = Any Amino Acid

<400> 469

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20 25 30

Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
35 40 45

Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
50 55 60

Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
65 70 75 80

Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
85 90 95

Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
100 105 110

Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
115 120 125

Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
130 135 140

Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
145 150 155

Ser Lys Gln Lys Asp Tyr Glu Glu Asp Ser Trp Asp Ser Glu Ser Lys

143

165

170

175

Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His
180 185 190

Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Ser Pro Asn
195 200 205

Lys Asp Gly Leu Leu Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro
210 215 220

Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro
225 230 235 240

Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser
245 250 255

Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala
260 265 270

Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser
275 280 285

Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val
290 295 300

Cys Leu Pro Lys Ala Xaa His Gln Lys Glu Ile Asp Lys Ile Asn Gly
305 310 315 320

Lys Leu Glu Gly Ser Pro Val Lys Asp Gly Leu Leu Lys Ala Asn Cys
325 330 335

Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met
340 345 350

Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro
355 360 365

Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys
370 375 380

Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys
385 390 395 400

Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu
405 410 415

Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Xaa His Gln Lys
420 425 430

Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp
435 440 445

Gly Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys
450 455 460

Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu
465 470 475 480

Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro
485 490 495

Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln
500 505 510

Met Phe Pro Ser Glu Ser Lys Gln Lys Xaa Val Glu Glu Asn Ser Trp
515 520 525

Asp Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val
530 535 540

Pro Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu
545 550 555 560

Glu Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys
565 570 575

Glu Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly
580 585 590

Lys Met Glu Gln Met Lys Lys Phe Cys Val Leu Lys Lys Lys Leu
595 600 605

Ser Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys
610 615 620

Trp Glu Gln Glu Leu Cys Ser Val Arg Phe Leu Thr Leu Met Lys Met
625 630 635 640

Lys Ile Ile Ser Tyr Met Lys Ile Ala Cys
645 650

<210> 470
<211> 228
<212> PRT
<213> Homo sapiens

<400> 470
Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys
5 10 15

Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys
20 25 30

Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
35 40 45

Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
50 55 60

145

Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
 65 70 75 80

Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
 85 90 95

Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
 100 105 110

Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe
 115 120 125

Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu
 130 135 140

Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu
 145 150 155 160

Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu
 165 170 175

Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His
 180 185 190

Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Lys Asn Arg
 195 200 205

Phe Leu Phe Lys Asn Gln Leu Thr Glu Tyr Phe Ser Lys Leu Met Arg
 210 215 220

Arg Asp Ile Leu
 225

<210> 471
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> (148)
<223> Xaa = Any Amino Acid

<400> 471
Met Arg Leu His Pro Trp Arg Lys Glu His Leu Thr Gln Leu Lys Ala
 5 10 15

Trp Trp Lys Lys His Leu Met Arg Leu His Pro Trp Trp Lys Glu His
 20 25 30

Leu Thr Arg Leu Lys Ala Trp Trp Lys Lys His Leu Met Arg Leu His
 35 40 45

146

Pro Trp Trp Arg Glu His Leu Thr Lys Phe Asn Val Trp Arg Lys Arg
 50 55 60

His Leu Glu Ser Ser Asn Ser Gln Gln Lys Lys His Leu Gly Lys Leu
 65 70 75 80

Arg Val Leu Gln Lys Lys His Leu Arg Asn Leu Arg Gly Gln Gln Lys
 85 90 95

Glu Asp Leu Gly Arg Ser His Gly Arg Lys Lys Met Thr Gln Leu Arg
 100 105 110

Gln Lys
 115 120 125

Lys
 130 135 140

Lys Lys Lys Xaa Lys Lys Lys Lys Lys
 145 150

<210> 472
<211> 467
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> (329)
<223> Xaa = Any Amino Acid

<400> 472
Met Ser Pro Ala Lys Glu Thr Ser Glu Lys Phe Thr Trp Ala Ala Lys
 5 10 15

Gly Arg Pro Arg Lys Ile Ala Trp Glu Lys Lys Glu Thr Pro Val Lys
 20 25 30

Thr Gly Cys Val Ala Arg Val Thr Ser Asn Lys Thr Lys Val Leu Glu
 35 40 45

Lys Gly Arg Ser Lys Met Ile Ala Cys Pro Thr Lys Glu Ser Ser Thr
 50 55 60

Lys Ala Ser Ala Asn Asp Gln Arg Phe Pro Ser Glu Ser Lys Gln Glu
 65 70 75 80

Glu Asp Glu Glu Tyr Ser Cys Asp Ser Arg Ser Leu Phe Glu Ser Ser
 85 90 95

Ala Lys Ile Gln Val Cys Ile Pro Glu Ser Ile Tyr Gln Lys Val Met
 100 105 110

Glu Ile Asn Arg Glu Val Glu Glu Pro Pro Lys Lys Pro Ser Ala Phe

115	120	125
Lys Pro Ala Ile Glu Met Gln Asn Ser Val Pro Asn Lys Ala Phe Glu		
130	135	140
Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Pro Met Phe Pro Pro Glu		
145	150	155
Ser Lys Gln Lys Asp Tyr Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu		
165	170	175
Cys Glu Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His		
180	185	190
Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asn		
195	200	205
Lys Asp Gly Leu Leu Lys Ala Thr Cys Gly Met Lys Val Ser Ile Pro		
210	215	220
Thr Lys Ala Leu Glu Leu Lys Asp Met Gln Thr Phe Lys Ala Glu Pro		
225	230	235
Pro Gly Lys Pro Ser Ala Phe Glu Pro Ala Thr Glu Met Gln Lys Ser		
245	250	255
Val Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala		
260	265	270
Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Asn		
275	280	285
Ser Trp Asp Thr Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val		
290	295	300
Cys Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly		
305	310	315
320		
Lys Leu Glu Gly Ser Pro Gly Lys Xaa Gly Leu Leu Lys Ala Asn Cys		
325	330	335
Gly Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met		
340	345	350
Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro		
355	360	365
Ala Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys		
370	375	380
Asn Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys		
385	390	395
400		
Gln Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu		
405	410	415

Thr Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Ala His Gln Lys
 420 425 430

Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Lys Asn Arg Phe Leu
 435 440 445

Phe Lys Asn His Leu Thr Lys Tyr Phe Ser Lys Leu Met Arg Lys Asp
 450 455 460

Ile Leu
 465

<210> 473

<211> 445

<212> PRT

<213> Homo sapiens

<400> 473

Lys Glu Ile Asp Lys Ile Asn Gly Lys Leu Glu Gly Ser Pro Val Lys
 5 10 15

Asp Gly Leu Leu Lys Ala Asn Cys Gly Met Lys Val Ser Ile Pro Thr
 20 25 30

Lys Ala Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro
 35 40 45

Glu Lys Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val
 50 55 60

Pro Asn Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp
 65 70 75 80

Glu Ile Leu Pro Ser Glu Ser Lys Gln Lys Asp Tyr Glu Glu Ser Ser
 85 90 95

Trp Asp Ser Glu Ser Leu Cys Glu Thr Val Ser Gln Lys Asp Val Cys
 100 105 110

Leu Pro Lys Ala Ala His Gln Lys Glu Ile Asp Lys Ile Asn Gly Lys
 115 120 125

Leu Glu Glu Ser Pro Asp Asn Asp Gly Phe Leu Lys Ala Pro Cys Arg
 130 135 140

Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
 145 150 155 160

Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
 165 170 175

Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
 180 185 190

Glu Gln Thr Leu Arg Ala Asp Gln Met Phe Pro Ser Glu Ser Lys Gln
195 200 205

Lys Lys Val Glu Glu Asn Ser Trp Asp Ser Glu Ser Leu Arg Glu Thr
210 215 220

Val Ser Gln Lys Asp Val Cys Val Pro Lys Ala Thr His Gln Lys Glu
225 230 235 240

Met Asp Lys Ile Ser Gly Lys Leu Glu Asp Ser Thr Ser Leu Ser Lys
245 250 255

Ile Leu Asp Thr Val His Ser Cys Glu Arg Ala Arg Glu Leu Gln Lys
260 265 270

Asp His Cys Glu Gln Arg Thr Gly Lys Met Glu Gln Met Lys Lys Lys
275 280 285

Phe Cys Val Leu Lys Lys Leu Ser Glu Ala Lys Glu Ile Lys Ser
290 295 300

Gln Leu Glu Asn Gln Lys Val Lys Trp Glu Gln Glu Leu Cys Ser Val
305 310 315 320

Arg Leu Thr Leu Asn Gln Glu Glu Lys Arg Arg Asn Ala Asp Ile
325 330 335

Leu Asn Glu Lys Ile Arg Glu Glu Leu Gly Arg Ile Glu Glu Gln His
340 345 350

Arg Lys Glu Leu Glu Val Lys Gln Gln Leu Glu Gln Ala Leu Arg Ile
355 360 365

Gln Asp Ile Glu Leu Lys Ser Val Glu Ser Asn Leu Asn Gln Val Ser
370 375 380

His Thr His Glu Asn Glu Asn Tyr Leu Leu His Glu Asn Cys Met Leu
385 390 395 400

Lys Lys Glu Ile Ala Met Leu Lys Leu Glu Ile Ala Thr Leu Lys His
405 410 415

Gln Tyr Gln Glu Lys Glu Asn Lys Tyr Phe Glu Asp Ile Lys Ile Leu
420 425 430

Lys Glu Lys Asn Ala Glu Leu Gln Met Thr Pro Arg Ala
435 440 445

<210> 474
<211> 221
<212> DNA
<213> Homo sapiens

<220>

150

<221> misc_feature
<222> (1)...(221)
<223> n = A,T,C or G

<400> 474

ggtccattcc tttcctcgcg tnggggttc tctgtgtca g cggccctcg tacactgatt 60
tccgatcaa agaatcatca tcttacatt gactttca g ggaattactg aactttcttc 120
tcagaagata gggcacagcc attgccttgg cctcaacttga agggtctgca tttgggtcct 180
ctggtctctt gccaagttt ccagccactc gagggagaaa t 221